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GenCore version 5.1.6
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- protein search, using sw model OM protein June 1, 2005, 11:37:44; Search time 128.533 Seconds (without alignments) 24.072 Million cell updates/sec Run on:

US-09-424-940A-2 50 1 GHRPLDKC 8 Title: Perfect score:

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2105692 segs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

2105692

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 16Dec04:* geneseqp1980s:* **Database**:

geneseqp1990s:* geneseqp200s:* geneseqp2001s:* geneseqp2003s:* geneseqp2003as:* geneseqp2003bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

tion	6 Human fib	7 Human fib	3 Fibrin-sp	0 Synthetic				9 Beta-pept	σ	1 Fibrinoge	9 Biotinyla	9 N-termina	9 Human fib	18 Human fib	6 Peptide W	Hun o	S.		S			7 Leukocyte	6 Leukocyte	0 Targeting	
Description	Aap82686	Aar44837	Aar65793	Aar63270	Aap71314	Aar0555	Aar65792	Aar63269	Abb7697	Aaw1193	Add32229	Aar28629	Aar44829	Aar44838	Abb78036	Aar4483	Aae3481	Aae34814	Aar40010	Add12888	Aao18333	Aar42547	Aar42546	Abp56240	Ade64331
QI	AAP82686	AAR44837	AAR65793	AAR63270	AAP71314	AAR05558	AAR65792	AAR63269	ABB76979	AAW11931	ADD32229	AAR28629	AAR44829	AAR44838	ABB78036	AAR44830	AAE34816	AAE34814	AAR40010	ADD12888	AA018333	AAR42547	AAR42546	ABP56240	ADE64331
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& Query Match Length	80	80	80	80	7	7	7	7	σ	10	11	12	12	12	14	16	20	25	28	28	28	29	30	30	30
% Query Match	100.0	100.0	100.0	100.0	82.0	82.0	82.0	82.0	82.0	82.0	82.0	82.0	82.0	82.0	82.0	82.0	82.0	82.0	82.0	82.0	82.0	82.0	82.0	82.0	82.0
Score	20	20	20	20	41	41	41	. 41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41
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Ω	Add69271 Human fib Add69272 Human fib
ADHS8575 ABB11339 AAG0151 AAC010151 AAC010778 AAC010150 AAM78493 ABM65149 ABM65149 ABM64478 ABM64481 ABM64482 ABM64482 ABM65482 ABM65481 ABM6548243 AARR62243	ADD69271 ADD69272
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ALIGNMENTS

RESULT 1

The peptide is linked to a carrier protein via a linking agent and used to immunise mice. The mouse spleen cells and amyeloma cell line can be fused to produce a hybridoma secreting MADS which bind specifically to human fibrin but not fibrinogen. (Updated on 25-MAR-2003 to correct PA New anti-human fibrin mono:clonal antibody, for diagnosing thrombosis prepd. from hybridoma obtd. by applying cell fusion mouse spleen and mouse myeloma-cells, and measures human fibrin. Fibrin; beta chain; N-terminal; monoclonal antibody; thrombosis. Human fibrin beta chain N-terminal. (MITN) MITSUBISHI GAS CHEM CO INC. AAP82686 standard; peptide; 8 AA. Claim 1; Page 1; 8pp; Japanese. 86JP-00237876. 86JP-00237876 (first entry) (revised) WPI; 1988-152086/22. Sequence 8 AA; JP63093800-A. 08-OCT-1986; 08-OCT-1986; 25-MAR-2003 05-DEC-1990 25-APR-1988 Synthetic. AAP82686; field.) AAP82686

Gaps ö Query Match

100.0%; Score 50; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 8; Conservative 0; Mismatches 0; Indels

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1 GHRPLDKC

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1 CHRPLDKC

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AAR65789-R65794 are synthetic peptides comprising fibrin-specific epitopic sequences, they can be used to prepare hybridoma cell lines, which produce antifibrin-specific monoclonal antibodies substantially devoid of fibrinogen cross-reactivity. These antibodies are useful in the in vivo and in vitro detection of thrombi and fibrin deposits. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                Synthetic epitopic peptide(s) of variable length - capable of eliciting fibrin specific antibodies free of fibrinogen cross-reactivity.
                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 50; DB 2; Length 8; 100.0%; Pred. No. 1.8e+06;
                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                    Claim 3; Col 18; 12pp; English.
                                                                             84US-00603155.
86US-00824228.
89US-00454954.
                                                        92US-00932729
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                                                                                                                                                    Haber
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                                                                                                                             (GEHO ) GEN HOSPITAL CORP.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                          8; Conservative
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                                                                                                                                                    Matsueda GR,
                                                                                                                                                                         WPI; 1994-332411/41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1994-358195/44
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                               1 GHRPLDKC
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GHRPLDKC
                                                                                                                                                                                                                                                                                                                                           Sequence 8 AA;
                                                        24-AUG-1992;
                                                                               23-APR-1984;
                                                                                            30-JAN-1986;
22-DEC-1989;
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           US5357042-A.
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21-JUL-1995
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                                  18-OCT-1994
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                                                                                                                                    Tissue plasminogen activator; t-PA; mutein; fibrin; antigen; anti-fibrin; monoclonal antibody; hybridoma; thrombolysis antithrombotic agent; bispecific antibody.
                                                                                                                                                                                                                                                                                                                                                     Hybrid monoclonal antibody - used for prepn. of thrombolytic having drug increased thrombolytic activity and specificity and reduced reactivity to
                                                                                                                                                                                                                                                                                                                                                                                                                            t
                                                                                                                                                                                                                                                                                                                                                                                                                        Human fibrin beta-chain peptides A and B were synthesised and coupled to BSA for injection into mice. The peptides were used to raise antibodies to human fibrin. Monoclonal antibodies specific for fibrin are used in the production of bispecific monoclonal antibodies which also recognise truncated tPA muteins lacking the finger, EGF and Kringle I domains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "May be absent and if present may be bonded
keyhole limpet hemocyanin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fibrin-specific epitopic peptides; thrombi detection; fibrinogen; antifibrin-specific monoclonal antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 50; DB 2; Length 8; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels
                                                                                                               Human fibrin beta-chain N-terminal peptide A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 14; 38pp; Japanese
                                          AAR44837 standard; peptide; 8 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR65793 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fibrin-specific epitopic peptide.
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                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                               WPI; 1993-408334/51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8 AA;
                                                                                                                                                                                                           JP05304992-A
                                                                                                                                                                                                                                                        17-JUN-1992;
                                                                                                                                                                                                                                                                                20-JUN-1991;
                                                                                        20-JUN-1994
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                                                                                                                                                                                                                                                                                                                                                                            fibrinogen.
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                                                                                                                                                                                     Synthetic.
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                                                                   AAR44837;
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Gaps

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0; Indels

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Inhibitor; thrombin; chimeric molecule; fibrin-binding; antibody; hirudin; monoclonal; 59D8; fibrinopeptide B; coagulation; P79; coronary stent implantation; adjunctive therapy; fibrinogen; haemorrhage.
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                                                                                                                                                                                                                                                                                                                                                                        Synthetic beta-peptide used to raise monoclonal antibody 59D8.
AAR63270 standard; peptide; 8 AA.
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Screening of fibrin-specific monoclonal antibodies - by contact with immobilised crosslinked fibrin clot and screening with detectable
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                                                            labelling step
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7 AA;
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11-OCT-1990
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AAR05558
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                                                                                                                               This sequence represents a synthetic beta-peptide which was used to immunopurify the monoclonal antibody 59D8 which was raised against beta-peptide (see also AR63269). The antibody binds fibrin and may be used in the chimeric molecule of the invention. The chimeric molecule further comprises a thrombin inhibitor linked to the fibrin-binding antibody through a covalent linkage. The chimeric molecule allows fibrin-specific antibody targetting of hirudin and other thrombin inhibitors, which is more potent than thrombin on its own. The epicope to which 59D8 binds becomes available only after thrombin cleaves fibrinopeptide B. The chimeric protein may be used for preventing coagulation of the blood. Anti-thrombin targetting can be esp. useful in highly thrombogenic situations such as coronary stent implantation and can be used as an adjunctive therapy with highly selective thrombin activity by the trombin inhibitor is localised to sites of thrombin activity by the antibody which binds to thrombin allows the total amount of fibrinogen. The selectivity of inhibition allows the total amount of thrombin inhibitor used to be substantially reduced, resulting in a produced thrombin inhibitor well and the substantially reduced. Tesulting in a produced to be substantially reduced, resulting in a produced to be substantially reduced. Tesulting in a produced the substantially resulting in a produced to be substantially resulting in a produced the substantially resulting in a produced the substantially resulting in a produced to stress the substant of the substantial produced to substantially resulting in a produced to substantially resulting in a produced to substantially resulting in a produced to be substantially resulting to the substantial substantial substantial substantial substantial substant and substantial substant and substant and substantial substanti
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preventing blood coagulation by specifically targetting inhibitor to site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reduced potential for generalised haemorrhaging. (Updated on 25-WAR-2003 to correct PN field.)
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                                                                                     Example 1; Page 14; 53pp; English
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(first entry)
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(GEHO ) GEN HOSPITAL CORP.
(GEHO ) GEN HOSPITAL CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
                              of thrombin activity
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Best Local Similarity
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                                             The MADS are specific to fibrin without fibrinogen cross-reactivity. They have increased binding to in vitro and in vivo thrombi. The MADS can be used in immunoassays for fibrin in the presence of fibrinogen or other proteins. They can be used as immunoaffinity ligands for the purification of fibrin. (Updated on 03-0CT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide is epitopic to fibrin, allowing anti-fibrin Abs to be raised without cross-reactivity to fibrinogen. They are particularly useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fibrin-specific monoclonal antibodies - lacking fibrinogen cross-reactivity, obtd. using peptide(s) comprising fibrin-specific epitopic
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         .
                                                                                                                                                                                                                                                                                                              ; DB 1; Lems.
/o. 1.8e+06; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fibrin; fibrinogen; thrombi; immunoaffinity.
                                                                                                                                                                                                                                                                                                                                     Query Match 82.0%; Score 41; DB Best Local Similarity 100.0%; Pred. No. 1.6 Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= His or Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Asp or Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Lys or Arg
Disclosure; Page 7; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR05558 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 17; 12pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          label= Leu or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86US-00824228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84US-00603155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide antigenic to fibrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matsueda BR, Haber E, Hui
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Matches

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us-09-424-940a-2.rag

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This sequence represents beta-peptide which was used to raise the monoclonal antibody 59BB. The antibody binds fibrin and may be used in the chimeric molecule of the invention. The chimeric molecule further comprises a thrombin inhibtor linked to the fibrin-binding antibody trapeting of hiradin and other thrombin inhibtors, which is nere potent than thrombin on its own. The epitope to which 59BB binds becomes available only after thrombin cleaves fibrinopeptide B. The chimeric protein may be used for preventing coaquiation of the blood. Anti-thrombin targetting can be esp. useful in highly thrombogenic situations such as coronary stent implantation and can be used as an adjunctive therapy with highly selective thrombin activity by the antibody which binds to thrombin but does not cross react with uncleaved fibrinogen. The selectivity of inhibition allows the total amount of thrombin inhibitor used to be substantially reduced, resulting in a reduced potential for generalised haemorrhaging. (Updated on 25-MAR-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fibrin-binding antibody linked to thrombin inhibitor - useful for preventing blood coagulation by specifically targetting inhibitor to site
                                                                                                                                     Inhibitor; thrombin; chimeric molecule; fibrin-binding; antibody;
hirudin; monoclonal; 59D8; fibrinopeptide B; coagulation; P79;
coronary stent implantation; adjunctive therapy; fibrinogen; haemorrhage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.0%; Score 41; DB 2; Length 7; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Residues 45-54 of human fibrinogen beta chain precursor.
                                                                                                   Beta-peptide used to raise monoclonal antibody 59D8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 13; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB76979 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                     94WO-US004881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bode C, Runge M;
                                         (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of thrombin activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1994-358195/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYEM-) UNIV EMORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GHRPLDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7 AA;
                                                                                                                                                                                                                                                         WO9425491-A1.
                                                                                                                                                                                                                                                                                                                                   03-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                         03-MAY-1993;
                                         25-MAR-2003
21-JUL-1995
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                                                                                                                                                                                                                   Synthetic.
       AAR63269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haber E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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ABB76979
ID ABB7
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AC ABB7
XX
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DT 22-J
XX
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DB Resi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           epitopic sequences, they can be used to prepare hybridoma cell lines, which produce antifibrin.specific monoclonal antibodies substantially devoid of fibrinogen cross-reactivity. These antibodies are useful in the in vivo and in vitro detection of thrombi and fibrin deposits. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic epitopic peptide(s) of variable length - capable of eliciting fibrin specific antibodies free of fibrinogen cross-reactivity.
detection of fibrin and thrombi. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR65789-R65794 are synthetic peptides comprising fibrin-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fibrin-specific epitopic peptides; thrombi detection; fibrinogen; antifibrin-specific monoclonal antibodies.
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                                                                                                                                     0; Indels
                                                                                             82.0%; Score 41; DB 2; Length 7; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.0%; Score 41; DB 2; Le
100.0%; Pred. No. 1.8e+06;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Fibrin-specific epitopic peptide.
                                                                                                                                                                                                                                                                                                             AAR65792 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR63269 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Col 18; 12pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84US-00603155.
86US-00824228.
89US-00454954.
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Best Local Similarity luv.v.
Best Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                     7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1994-332411/41
                                                                                                                                                                         1 GHRPLDK 7
                                                                                                                 Best Local Similarity
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GHRPLDK 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GHRPLDK 7
                                                                                                                                                                                                 GHRPLDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7 AA;
                                                         Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-APR-1984;
30-JAN-1986;
22-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
26-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5357042-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                   AAR65792;
                                                                                                 Query Match
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RESULT 7
ARR65792
ARR66792
ARR66793
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Gaps

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AAR63269 ID AAR6 XX

RESULT 8

not with

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antirheumatic; antiinflammatory; antiarthritic; peptide therapy;
proinflammatory; tetrapeptide; inflammation; synovial joint inflammation;
rheumatoid arthritis; fibrinogen A alpha chain; fibrin polymerisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes a method of inducing proinflammatory effects in synovial or fibroblast cells comprising exposing the cells to a specific tetrapeptide (GPRP) peptide (I). (I) is used for inducing proinflammatory effects in synovial or fibroblast cells. An analogue of (I) is used for treating or preventing inflammation of a synovial joint or rheumatoid arthritis in a subject. (I) is used to identify a receptor for (I) comprising exposing several fibroblastic cells or synovial cells to (I).
                                                                                                                                    not with human fibrinogen. Specifically when the MAb reacts with ureatreated des-AABB fibrin the reaction is not inhibited by peptides corresponding to fibrinogen A-alpha-chain residues 17-26 (AAW11931), B-beta-chain residues 15-24 (AAW11932) or gamma-chain residues 312-324 (AAW11933). The MAb is useful in immunoassays for soluble fibrin in plasma samples (e.g. by sandwich immunoassay), particularly for the diagnosis of pathological conditions such as disseminated intravascular
                                                                                                                           novel monoclonal antibody (MAb) reacts with human soluble fibrin, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inducing proinflammatory effects in human synovial or fibroblast cells comprises using a specific tetrapeptide which can also identify a receptor to the tetrapeptide.
                                              Monoclonal antibody reactive with soluble human fibrin - but not fibrinogen, is useful for fibrin immunoassay in plasma specimens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biotinylated fibrin polymerisation associated control peptide.
                                                                                            Example 3; Page 15; 32pp; Japanese.
                                                                                                                                                                                                                                                                                                 82.0%; Scc.
100.0%; Pred
0; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADD32229 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-AUG-2001; 2001US-00931009.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-AUG-2001; 2001US-00931009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                             Conservative
                WPI; 1995-206667/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-829401/77.
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                        GHRPLDK 7
                                                                                                                                                                                                                                                                                                                                                                                              GHRPLDK 7
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                                                                                                                                                                                                                                                                                Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                     coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADD32229;
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                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a citrulline (Cit) containing polypeptide derived from all or part of the alpha- or beta-chains of fibrin by substitution of at least one arginine residue by Cit. The Cit containing polypeptides can be used for in vitro diagnosis of rheumatoid polyperthritis (RP), by detecting disease-specific autoantibodies, and therapeutically for neutralising the RP-associated autoimmune response. The present sequence is a fragment (residues 45-54) of the human fibrinogen beta chain precursor, which was used in an example from the
                                                                                                                                                                                                                                                                                                           citrulline-containing polypeptide from fibrin, useful for diagnosis treatment of rheumatoid polyarthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monoclonal; antibody; human; soluble; fibrin; fibrinogen; urea-treated; des-AABB; A-alpha-chain; immunoassay; diagnosis;
                anti-inflammatory; fibrin; rheumatoid polyarthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.0%; Score 41; DB 4; Length 9; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fibrinogen A-alpha-chain residues 17-26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disseminated intravascular coagulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kohno I, Inuzuka K, Ito Y;
                                                                                                                                                                                                                 (UYTO-) UNIV TOULOUSE SABATIER PAUL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW11931 standard; peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 12; 23pp; French
                                                                                                                                                      99FR-00008470.
                                                                                                                                                                                   99FR-00008470.
                              human; fibrinogen beta chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94WO-JP001844
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                                                                                                                                                                                                                                                                             WPI; 2001-114394/13
                                                                                                                                                                                                                                             Serre G, Sebbag M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                Anti-arthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9 AA;
                                                            Homo sapiens
                                                                                        FR2795735-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-NOV-1993;
                                                                                                                                                      01-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9512617-A1
                                                                                                                        05-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention
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Gaps

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Length 10; 0; Indels

DB 2; 0.15;

Mismatches Score 41; Pred. No.

us-09-424-940a-2.rag

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WPI; 1993-408334/51.
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                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                   JP05304992-A.
                                                                                                                                                                                                                                                                            17-JUN-1992;
                                                                                                                                                                                                                                                                                                20-JUN-1991;
                                                               20-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JUN-1994
                                                                                                                                                                                                                                                       19-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                   fibrinogen.
                                                                                                                                                 Synthetic
                                           AAR44829;
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                                                                                                                                                                                Region
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Matches
   RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bi:specific antibody useful for treating thrombotic obstructive diseases e.g. cardiac infarction - comprises antibrombus antibody variable region and anti-thrombolytic substance antibody variable region with no heavy chain constant region domains 2 and 3.
(I) Can identify, isolate and clone the cell receptor to which it binds. This is the amino acid sequence of a control peptide associated with the ihibition of fibrin polymerisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents an N-terminal peptide of human fibrin. It was used in the production of bispecific monoclonal antibodies which are specific for fibrins, but do not bind fibrinogen, and and are specific for anti-thrombolytic substance. The compsn. contg. these Abs lacks the side effects of prior art Ab targetted thrombolytic agents and has enhanced thrombolytic actvity. (Updated on 25-MAR-2003 to correct PN
                                                                                    Gaps
                                                                                                                                                                                                                                                                          bispecific hybrid monoclonal antibody; thrombolytic agent;
cardiac infarction; arterial embolism; cerebral infarction;
peripheral arterial/venous obstruction; retinal arterial obstruction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.0%; Score 41; DB 2; Length 12; 100.0%; Pred. No. 0.18; ive 0; Mismatches 0; Indels
                                                              DB 7; Length 11;
0.16;
                                                                                   0; Indels
                                                            82.0%; Score 41; DB 100.0%; Pred. No. 0.1 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Watanabe A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Page 3; 30pp, English.
                                                                                                                                                                               AAR28629 standard; peptide; 12 AA
                                                                                                                                                                                                                                                      N-terminal human fibrin peptide.
                                                                                                                                                                                                                                                                                                                                                                                  92EP-00108134.
                                                                                                                                                                                                                                                                                                                                                                                                      91JP-00112874.
                                                                                                                                                                                                                                                                                                                                                                                                                                    (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                   (first entry)
                                                                        Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                        (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Iwasa S, Kurokawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1992-383677/47.
                                                                                                     GHRPLDK 7
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les 7; Conserv
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                                                                                                                    GHRPLDK
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                                          Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12 AA;
                                                                                                                                                                                                                      25-MAR-2003
22-MAR-1993
                                                                                                                                                                                                                                                                                                                    Ното варіеля
                                                                                                                                                                                                                                                                                                                                                                                 14-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                      17-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAR-1992;
                                                                                                                                                                                                                                                                                                                                        EP513778-A2.
                                                                                                                                                                                                                                                                                                                                                             19-NOV-1992
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                                                                                                                                                                                                    AAR28629;
                                                              Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue plasminogen activator; t-PA; mutein; fibrin; antigen; anti-fibrin; monoclonal antibody; hybridoma; thrombolysis antithrombotic agent; bispecific antibody.
                                                                                                                                                                                               Tissue plasminogen activator; t-PA; mutein; fibrin; antigen; anti-fibrin; monoclonal antibody; hybridoma; thrombolysis antithrombotic agent; bispecific antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hybrid monoclonal antibody - used for prepn. of thrombolytic having drug increased thrombolytic activity and specificity and reduced reactivity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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    .11 human fibrin beta-chain residues 1-11"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "BSA carrier is attached to Cys"
                                                                                                                                                  Human fibrin beta-chain N-terminal peptide (1-11)-Cys.
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                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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AAR44829 standard; peptide; 12 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92JP-00158301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91JP-00148936
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                                                                                                 (first entry)
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Hybrid monoclonal antibody - used for prepn. of thrombolytic having drug increased thrombolytic activity and specificity and reduced reactivity to
                                                                                                                                                                                                                                                             Human fibrin beta-chain peptides A and B were synthesised and coupled to BASA for injection into mice. The peptides were used to raise antibodies to human fibrin. Monoclonal antibodies specific for fibrin are used in the production of bispecific monoclonal antibodies which also recognise truncated tPA muteins lacking the finger, EGF and Kringle I domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel peptides acting as modulators of fibrin fragment B activity for treating disease responding to stimulation or inhibition of cell proliferation or angiogenesis e.g. wound healing, ischemia, cancer and
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fibrin beta chain; fibrinogen beta chain; fibrin fragment B; cell proliferation; angiogenesis; fibrogenesis; collagen synthesis; wound healing; skin graft; heart muscle revascularisation; linb replacement; ischaemia; scarring; restenosis; atherogenesis; rheumatoid arthritis; diabetes; renal disease; psoriasis; macular degeneration; cancer; fibrin glue; stent; angioplasty; antennapedia protein; membrane translocation.
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                                                                                                                                                                                                                                                                                                                                                                                Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide WTM250 derived from fibrin/fibrinogen beta chain.
                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                    82.0%; Scor.
100.0%; Pred. No. v...
0; Mismatches
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                                                                                                                                                                                                                                     Example 1; Page 14; 38pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB78036 standard; peptide; 14 AA.
                                                                                             91JP-00148936.
                                                                    92JP-00158301
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                                                                                                                       (TAKE ) TAKEDA CHEM IND LTD
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                                                                                                                                                                                                                                                                                                                                                                                                          7; Conservative
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                                                                                                                                                  WPI; 1993-408334/51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             GHRPLDK 12
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    GHRPLDK
                                                                                                                                                                                                                                                                                                                                                    Sequence 12 AA;
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             JP05304992-A
                                                                  17-JUN-1992;
                                                                                             20-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-JUN-2002.
                                     19-NOV-1993
                                                                                                                                                                                                          fibrinogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
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The specification describes peptides which correspond to portions of fibrin fibrin/fibrinogen beta chain sequences, and act as modulators of fibrin fragment B activity, and in turn modulators of fibrin E effects. Such effects include induction of cell proliferation, angiogenesis, confidence in an expension of the peptides are used for wound heart muscle or limb replacement surgery. They are also used for treating ischaemia, reduction of scarring, and prevention of restenosis. The peptides may also be used for treating atherogenesis, rheumatoid arthritis, diabetes, renal disease, psoriasis, macular degeneration, or cancer. The peptides are also useful for modifying fibrin glues, and may be incorporated into a stent which is introduced into the arteries of the patient during an angioplasty procedure for preventing restenosis.

ABB78036-38 represent peptides derived from fibrin/fibrinogen beta chain sequences. The peptides are derived from the region where plasmin cleaves the molecule, and contain a Ceterminal Cys which does not appear in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tissue plasminogen activator; t-PA; mutein; fibrin; antigen; anti-fibrin; monoclonal antibody; hybridoma; thrombolysis antithrombotic agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lybrid monoclonal antibody - used for prepn. of thrombolytic having drug nicreased thrombolytic activity and specificity and reduced reactivity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human fibrin internal peptide fragment was identified as a candidate immunogen to raise antibodies to human fibrin. Monoclonal antibodies specific for fibrin are used in the production of bispecific monoclonal antibodies which also recognise truncated tPA muteins lacking the finger,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                         Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human fibrin beta-chain internal peptide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                         DB 5;
0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Page 9; 38pp; Japanese.
                                  Example 3; Page 46; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR44830 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                       82.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1993-408334/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bispecific antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                    wild type protein
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14 AA;
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Best Local
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Matches
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Sequence 25 AA;
                                                                         WO200292117-A1.
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Modified-site
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23-MAY-1994
                                                                                           21-NOV-2002
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                                                                                                                                                                    Davis S,
                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 19
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                                                                                                                                                                                                                                                                                                                                                                                  Treating or preventing thrombin-induced coagulation of blood for treating a disease condition such as stroke, myocardial infarction, sickle-cell crisis or venous thrombosis by administering a SdrG protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a method for treating or preventing thrombin-
induced coagulation of blood by administering a SdrG protein. The method
is sued for preparing a composition for treating myocardial infarction,
stroke, sickle-cell crisis or venous thrombosis. The present sequence is
Staphylococcus epidermidis fibrinogen (Fg) Bbeta chain peptide used to
illustrate the method of the invention
                                                                                                                                                                                             Thrombin-induced blood coagulation; myocardial infarction; SdrG protein; sickle-cell crisis; venous thrombosis; stroke; therapy; anticoagulant; fibrinogen; Fg.
                                    Gaps
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0
                                                                                                                                                                           epidermidis fibrinogen (Fg) Bbeta chain peptide, beta6-25.
                  Length 16;
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                                    0; Indels
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                 82.0%; Score 41; DB 2;
100.0%; Pred. No. 0.24;
ive 0; Mismatches
                                                                                                                      AAE34816 standard; peptide; 20 AA.
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                                                                                                                                                                                                                                                                                                                           (TEXA ) UNIV TEXAS A & M SYSTEM
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                                                                                                                                                                                                                                                                                                           11-MAY-2001; 2001US-0290072P
                 82.0%;
                                                                                                                                                                                                                                   Staphylococcus epidermidis.
                                                                                                                                                          (first entry)
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                           Best Local Similarity 100 Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-140257/13.
                                                                        GHRPLDK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GHRÞĽDK 16
                                                                                                                                                                                                                                                                                                                                               HOOK MAO;
                                                       GHRPLDK 7
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les 7; Conser
Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 AA;
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                                                                                                                                                          28-MAY-2003
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                  Query Match
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AAE34814
ID AAE34!
XX
AC AAE34!
XX
DT 28-MA'
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Matches
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Treating or preventing thrombin-induced coagulation of blood for treating a disease condition such as stroke, myocardial infarction, sickle-cell crisis or venous thrombosis by administering a SdrG protein.
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induced coagulation of blood by administering a SdrG protein. The method
is sued for preparing a composition for treating myocardial infarction,
stroke, sickle-cell crisis or venous thrombosis. The present sequence is
Staphylococcus epidermidis fibrinogen (Fg) Bbeta chain peptide used to
illustrate the method of the invention
                                           Thrombin-induced blood coagulation; myocardial infarction; SdrG protein; sickle-cell crisis; venous thrombosis; stroke; therapy; anticoagulant; fibrinogen; Fg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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    S. epidermidis fibrinogen (Fg) Bbeta chain peptide, betal-25.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scintigraph imaging agent specific binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.0%; Score 41; DB 6;
100.0%; Pred. No. 0.39;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR40010 standard; peptide; 28 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Col 19; 29pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TEXA ) UNIV TEXAS A & M SYSTEM.
                                                                                                                                                                                                                                                                                                                                                          13-MAY-2002; 2002WO-US014741
                                                                                                                                                                                                                                                                                                                                                                                                                        11-MAY-2001; 2001US-0290072P.
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                                                                                                                                                                             Staphylococcus epidermidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 82.0
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-140257/13
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                                                              Reagents for preparing scintigraphic imaging agents - contg. technetium-
99M labelled peptide(s) contg. 3-100 aminoacid(s).
                                                                                                                   The sequence is that of a specific binding peptide used as part of a reagent for preparing a scintigraphic imaging agent for imaging sites within a mammalian body. In this the peptide is covalently linked to a radiolabel-binding moiety which is capable of forming a complex with a radiolsocope, pref. technetium-99M. (Updated on 25-MAR-2003 to correct field.) (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                imaging; scintigraphic imaging agent; SIA; Technetium-99m; tumour; somatostatin receptor; leukocytes; atherosclerotic plaque;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scintigraphic imaging agent comprising specific binding peptide attached via an amino acid side chain to a radio:label binding gprovides rapid imaging of tumours, thrombosis etc.
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                     Civitello
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                                                                                                                                                                                                                     Length 28;
                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            scintigraphic imaging agent associated peptide #12
                     Lister-James J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lister-James J,
                                                                                                                                                                                                                    Score 41; DB 2;
Pred. No. 0.45;
                                                                                                                                                                                                             82.0%; Sco...
100.0%; Pred. No. v...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                         ADD12888 standard; peptide; 28 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 14; Page 34; 43pp; English
                    Mcbride W,
                                                                                              Claim 35; Page 39; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mcbride W,
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                                                                                                                                                                                                                               Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    deep vein thrombosis.
                    Dean RT, Buttram S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dean RT, Buttram S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-039983/04.
                                          WPI; 1993-368429/46
(DIAT-) DIATECH INC
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                                                                                                                                                                                                                                                               1 GHRPLDK 7
                                                                                                                                                                                                                                                                                     GHRPLDK
                                                                                                                                                                                                Sequence 28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09533498-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-DEC-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                ADD12888;
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8XCCCCCX8X77X8X7CCCCX8
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tumours that express somatostatin receptors; leukocytes; atherosclerotic blaque; and deep vein thrombosis. Attachment of (II) to a sidechain avoids any interference with the specific binding proparties of (I) and makes possible derivatisation of cyclic peptides (which are more resistent to proceolysis). Images may be recorded only a few minutes after injection of SIA. This is the amino acid sequence of a peptide associated with the imaging methods of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rheumatic disease; organ transplantation; arteriosclerosis; reperfusion trauma; thrombosis; cancer; antiinfammatory; antibacterial; immunosuppressive; antirheumatic; antiarteriosclerotic; vasotropic; thrombolytic; anticosqulant; cytostatic; antipsoriatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptides or proteins based on fibrin or fibrinogen sequences, useful combating fibrin-mediated disorders such as inflammation, transplant rejection, arteriosclerosis and reperfusion damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fibrin; fibrinogen; antagonist; inflammation; autoimmune disease;
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psoriasis. The present sequence is a peptide of the invention
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                                                                                                                                                                                                                                                                                                                                                            Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                         DB 2;
. 0.45;
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0.45;
                                                                                                                                                                                                                                                                                                                                                     82.0%; Score 41; DB 100.0%; Pred. No. 0.4 iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fibrinogen based therapeutic peptide #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.0%; Score 41; 100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAO18333 standard; peptide; 28 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 5; Page 40; 41pp; German
                                                                                                                                                                                                                                                                                                                                                                                             Similarity 100.0%; 7; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-DEC-2000; 2000AT-00002063
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Best Local Similarity
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Matches 7; Conserv
                                                                                                                                                                                                                                                                                      Sequence 28 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-JUN-2002
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us-09-424-940a-2.rag

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                                                                                                                                                                                                                                                                      Buttram S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP56240 standard; peptide; 30
                                                                                                                                                                                                                93WO-US002320
                                                                                                                                                                                                                                 92US-00851074
                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                          /note=
                            (revised)
                                                                                                                                                                                                                                                                                     WPI; 1993-303154/38.
                                                                                                                                                                                                                                                   (DIAT-) DIATECH INC
                                                                                                                                                                                                                                                                     Lees RS,
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ses 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 30 AA;
                                                                                                                      Key
Modified-site
                                                                                                                                               Modified-site
                                                                                                                                                                                                               12-MAR-1993;
                                                                                                                                                                                                                                 13-MAR-1992;
                                                                                                                                                                            WO9317719-A1
                            25-MAR-2003
                                     05-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-MAR-2003
                                                                                                                                                                                              16-SEP-1993
                                                                                                    Synthetic.
           AAR42546;
                                                                                                                                                                                                                                                                   Dean RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              New peptides are claimed which are leukocyte binding peptides having covalently bound to them a moiety which can bind a Tc-99m radiolabel. The peptides having Tc-99m bound to them are useful as scintigraphic imaging agents for imaging sites of infection and inflammation in the mammalian body, e.g. caused by ischaemia, inflammatory bowel disorder, arthritis or tumours. The present sequence is a specifically claimed example of such a peptide derived from fibrinopeptide B chain. (Updated on 25-MAR-2003 to
                                                                                                                                                                Leukocyte binding peptide; fibrinopeptide B chain; scintigraphic imaging; inflammatiom site; technetium 99m.
                                                                                                                                                                                                                                         /note= "BAT, i.e. N6,N9-bis(2-methyl- 2-mercaptopropyl)-6,9-diazanonanoic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   Scintigraphic imaging agent for sites of inflammation - comprising leukocyte-binding peptide bound technetium-99m via binding moiety.
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                                                                                                                                               Leukocyte-binding peptide which can bind to technetium-99m.
0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                 Lister-James J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
0.46;
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100.0%; Pred. No. vo...
0; Mismatches
Mismatches
                                                                                                                                                                                                              Location/Qualifiers
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AAR42546
ID AAR42546 standard; peptide; 30 AA.
                                                                               AAR42547 standard; peptide; 29 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 15; Page 31; 40pp; English
°,
                                                                                                                                                                                                                                                                    /note= "Arg-NH2
                                                                                                                                                                                                                                                                                                                                                                               Dean RT, Lees RS, Buttram S,
                                                                                                                                                                                                                                /label= OTHER
                                                                                                                                                                                                                                                                                                                           93WO-US002320
                                                                                                                                                                                                                                                                                                                                             92US-00851074
                                                                                                                             (first entry)
7; Conservative
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                                                                                                                     (revised)
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                 GHRPLDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 29 AA;
                                                                                                                                                                                                              Key
Modified-site
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                                                                                                                                                                                                                                                                                                                          12-MAR-1993;
                                                                                                                                                                                                                                                                                                                                           13-MAR-1992;
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                                                                                                                                                                                                                                                                                                         16-SEP-1993;
                                                                                                                   25-MAR-2003
05-AUG-1994
                                                                                                   AAR42547;
                                                                                                                                                                                            Synthetic
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Matches
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                                                               RESULT 22
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                                                         Leukocyte binding peptide; fibrinopeptide B chain; scintigraphic imaging; inflammatiom site; technetium 99m.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scintigraphic imaging agent for sites of inflammation - comprising leukocyte-binding peptide bound technetium-99m via binding moiety.
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0
Leukocyte-binding peptide which can bind to technetium-99m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lister-James J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
0.48;
                                                                                                                                                                                                                                                                                                                                                       "acetamidomethyl-Cys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.0%; Score 41; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                       /note= "picolinoyl-Gly"
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                                                                                                                                                                                                                          Location/Qualifiers
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Pearson DA;
                                                                                                            (CYRJ/) CYR J E.
(PEAR/) PEARSON D A.
                                                                                                                                                                   WPI; 2004-040976/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                1 GHRPLDK
            US2003072709-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CYRJ/) CYR J E.
                                                                                                                                                                                                                                                                                                                                                              Sequence 30 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2003103895-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2004
                                 17-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADH58575;
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                             Cyr JE,
                                                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADH58575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a composition (C) comprising a radiopharmaceutical precursor and a stabiliser selected from hydrophilic thioether (I) and/or hydrophilic 6-hydroxy-chroman derivative (II). Also described: (1) stabilising a radiopharmaceutical comprising; combining the radiopharmaceutical precursor with (1) and/or (II) in a container, and adding a radionuclide to the container; and (2) a kit comprising a sealed vial containing the radiopharmaceutical precursor, and (I) and/or (II). (C) can be used to increase the shelf life of diagnostic and therapeutic radiopharmaceutical precursors in nuclear medicine. The stabilisers maintain the radiochemical purity of the radiopharmaceutical containing a vide variety of radiopharmaceutical. (C) is suitable for stabilishing a wide variety of radiopharmaceuticals. The present sequence represents a specifically contained targeting moiety peptide for a composition from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                        Composition useful for increasing shelf life of diagnostic and therapeutic radiopharmaceuticals, comprising radiopharmaceutical precursor and hydrophilic thioether and/or hydrophilic 6-hydroxy-chroman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Radiopharmaceutical composition stabilising hydrophilic thioether #5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          radiopharmaceutical precursor; hydrophilic thioether;
radiopharmaceutical composition; diagnosis; therapy; shelf life;
diagnostic radiopharmaceutical; therapeutic radiopharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.0%; Score 41; DB 6; Length 30;
100.0%; Pred. No. 0.48;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "C-terminal amide"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADE64331 standard; peptide; 30 AA.
                    /note= "amidated
                                                                                                                                                                                                                                                                                 Claim 15; Page 48; 64pp; English
                                                                                                         24-OCT-2000; 2000US-00694992.
24-OCT-2000; 2000US-00695360.
24-OCT-2000; 2000US-00695494.
                                                                                     24-OCT-2001; 2001WO-US050423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.vv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                             Pearson DA;
                                                                                                                                                       (DIAT-) DIATIDE INC.
                                                                                                                                                                                                   WPI; 2003-092782/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GHRPLDK 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 30 AA;
                                         WO200260491-A2
          Modified-site
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Modified-site
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                                                                 08-AUG-2002
                                                                                                                                                                                                                                                          derivative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADE64331;
                                                                                                                                                                              Cyr JE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                radiopharmaceutical precursor; hydrophilic 6-hydroxy-chroman derivative; stabiliser; radiopharmaceutical composition; diagnosis; therapy; shelf life.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 13; SEQ ID NO 5; 19pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADH58575 standard; peptide; 30 AA.
24-APR-2002; 2002US-00131543.
                                                               24-OCT-2000; 2000US-00694992.
24-OCT-2001; 2001WO-US050423.
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24-OCT-2001; 2001WO-US050423
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                                                                                                                                                                                                                  The invention describes a composition comprising a radiopharmaceutical precursor and a hydrophilic 6-hydroxy-chroman derivative. The composition is useful as stabilisers of radiopharmaceutical compositions for use in
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                                                                                                                                                                                                                                                                     diagnosis and therapy. The composition is particularly useful for increasing the shelf life of diagnostic or therapeutic radiopharmaceuticals. This is the amino acid sequence of a peptide used in the stabilisation of radiopharmaceutical compositions.
                                                                                                 Compositions, useful as stabilizers, or for increasing shelf life, of radiopharmaceuticals for use in diagnosis or therapy, comprises radiopharmaceutical precursor, hydrophilic thioether and hydrophilic 6-hydroxy-chroman derivative,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          haematopoiesis regulation, tissue growth, immunomodulator; activin, inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bone disorder; osteoporosis; vascular growth disorder;
tissue regeneration; wound healing; infection; immune disorder;
cell culture; drug screening; gene therapy; antiinflammatory;
antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                         82.0%; Score 41; DB 8; Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human beta-fibrinogen homologue, SEQ ID NO:1709.
                                                                                                                                                                                                                                                                                                                                                                                                           0.48;
                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Fred.
                                                                                                                                                                                 Claim 16; SEQ ID NO 5; 17pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB11339 standard; peptide; 87 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antifungal; vulnerary; antiulcer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fang YT, Liu C, Drmanac RT;
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27-APR-2000; 2000US-00560875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
1es 7; Conservative
PEARSON D A.
                                  Pearson DA;
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                                                                  WPI; 2004-106449/11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          GHRPLDK 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ABA08583
                                                                                                                                                                                                                                                                                                                                                        Sequence 30 AA;
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                                                                                                                                                                                                                                                                                                                                                                                      Query Match
 (PEAR/)
                               Cyr JE,
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ABB11339
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Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides.

Conclectide of the invention, methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence of potential therapeutic applications. The polypeptides of the invention may have various activities, into their probable biological activities, and hence differentiation activities, sem cell growth factor activity; lampare activity; insue growth activity; concentration activities, repeated activities, concentration and activities, or may or activities; or may or activities; and mencertain and activities, polypeptides and mucleotides of thrombolytic activities, receptor or ligand activities; or may be used in oncogenesis, cancer cell proliferation or metastasis.

Conditions, e.g., by protein or gene therapy, Such conditions include cancers, hematopotetic disorders (e.g., metopoted call activities propertions or ameliorating medical carterial ischemia, bone disorders (e.g., metopotes), chronic inflammatory conditions (e.g., asthma or arthitis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischemia, bone disorders (e.g., metopotes), will exhemia benearial benearial and disorders (e.g., metopotes) will carterial and fungal infections in addition to immune disorders to manipulate stem cells incitive may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorder set or equation and engage to manipulate stem cells in our properties and prope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                         Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; 5' BST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human secreted protein, SEQ ID NO: 4232.
                                                                                                                  Claim 20; Page 167; 1963pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG00151 standard; protein; 118 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptide of the invention
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 87 AA;
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                                                                         and cancer.
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셤
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EP1033401-A2.

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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent of or puse in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to easies also useful for producing the proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon stimulation; as anti-inflammatory agents; and in treatment of leuxaemias. AAUS9510-AAUS3304 represent the amino acid sequences of novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                               Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; SEQ ID NO 24670; 1399pp + Sequence Listing; English
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2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.0%; Score 41; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA010778 standard; protein; 141 AA.
                                                                                               Claim 20; Page 752; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          secreted proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human polypeptide SEQ ID NO 24670.
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18-MAY-2000; 2000US-00577409.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-514838/56.
WPI; 2001-611725/70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45 GHRPLDK 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AA190709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 140 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200164835-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAO10778;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA010778
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                                                                                                                                                                                                                                                                                                                                                                        The present sequence is a polypeptide encoded by one of a large number of 5. ESTB derived from mRNAs encoding secreted proteins. The 5. ESTB were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTB are not well suited for isolating cDNA sequences derived from the STB are not well suited for isolating cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTB are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTB are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, vaccination, gene therapy, nutritional supplement,
stem cell proliferation, haematopoiesis, nerve tissue regeneration,
immune suppression, immune stimulation, anti-inflammatory, leukaemia.
                                                                                                                                                                                                                                                        New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.0%; Score 41; DB 3; Length 118; 100.0%; Pred. No. 2.1; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                       Claim 13; SEQ ID NO 4232; 71pp + Sequence Listing; English
                                                                                                                                                         Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and to design expression and secretion vectors
                                                                                                                                                         Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU33273 standard; protein; 140 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human secreted protein #3764.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rang YT, Liu C, Drmanac RT;
                                   21-FEB-2000; 2000EP-00200610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-APR-2000; 2000US-00552929
26-JAN-2001; 2001US-00770160
                                                                          99US-0122487P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 82.0
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                         Dumas Milne Edwards J,
                                                                                                                                                                                                WPI; 2000-500381/45
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45 GHRPLDK 51
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                                                                                                                                                                                                                     N-PSDB; AAC00157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200179449-A2
                                                                                                                 (GEST ) GENSET
                                                                          26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell prollferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity, insue growth factor activity, and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a polypeptide encoded by one of a large number of 5' ESTS derived from mRNAs encoding secreted proteins. The 5' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated primed cDNA libraries. Such ESTS are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where included. S' ESTs are derived from mRNAs with intact 5' ends and earling cDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
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                                                                                                                                                                                                                                                                                                                                        Score 41; DB 4; Length 141;
Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                              100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted protein, SEQ ID NO: 4231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG00150 standard; protein; 150 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene therapy; chromosome mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-FEB-2000; 2000EP-00200610.
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                                                                                                                                                                                                                                                                                                                                        82.08;
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100....
7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-500381/45.
N-PSDB; AAC00156.
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GHRPLDK 47
                                                                                                                                                                                                                                                                                                                                                                                                                 CHRPLDK 7
                                                                                                                                                                                                                                                                                             Sequence 141 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GEST ) GENSET
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 mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                  Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xu C, Cao Y;
, Chen R, Wang ZW;
                                                                                                                    Gaps
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0
                                                                                 DB 3; Length 150; 2.7;
                                                                                                                  0; Indels
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J, Zhang J, Ren F,
Goodrich R;
                                                                               82.0%; Score 41; DB 100.0%; Pred. No. 2.7 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; Page 3390-3391; 6221pp; English.
                                                                                                                                                                                                                                                                 AAM78493 standard; protein; 453 AA.
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Wejhrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu C, Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                    Human protein SEQ ID NO 1155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-FEB-2001; 2001WO-US004098.
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27-APR-2000; 2000US-00560875.
20-JUN-2000; 2000US-00598075.
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20-OCT-2000; 2000US-00693325.
30-NOV-2000; 2000US-00728422.
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01-SEP-2000; 2000US-00654936
                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                  7; Conservative
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                                                                                                                                                                                  51
                                                                               Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                 1 GHRPLDK 7
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                                                                                                                                                                                  45 GHRPLDK
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Xue AJ, Yang Y,
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                                                Sequence 150 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                    RESULT 32
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8; Length 455;

Sequence 455 AA;

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The invention relates to novel diagnostic and therapeutic polymucleotides selected from one of the 2722 sequences defined in the specification. A purincleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polymucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine of autoimmune/inflammatory disorder, developmental disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp conflections caused by virus, bacteria, fungi or parasite. The dithp conflections caused by virus, bacteria, fungi or parasite. The dithp conflections any also be used in genetic mapping, in identifying individuals confluent may laso be used in genetic mapping, in identifying individuals confluent may be used in genetic mapping, in identifying individuals confluent may be present sequence represents a dithp protein of the gene therapy. The present sequence represents a dithp protein of the gene therapy. The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wright RJ, Bruns CM, Marjanovic MM, Shen F;
TA, Suchorolski MT, Altus CM, Pitts SJ, Blder LV;
Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Blanchard JL, Panezer SR, Wang X, Au AP, Gerstin EH;
Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
G M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
Shi X, Suarez CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
                                                                          Gaps
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                                 82.0%; Score 41; DB 4; Length 453; 100.0%; Pred. No. 8.9; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                               Human diagnostic and therapeutic pprotein SEQ ID NO:5398.
                                                                                                                                                                                                                                                         ABM85149 standard; protein; 455 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-SEP-2002; 2002US-0410259P.
12-SEP-2002; 2002US-0410260P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-SEP-2003; 2003WO-US028227.
                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                     Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                        |||||||||||||GHRPLDK 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kwong M, Po
S, Shi X,
                                                                                                                  1 GHRPLDK 7
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Sequence 453 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2004023973-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene mapping
                                                                                                                                                                                                                                                                                                                                       18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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Peralta CH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2004.
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                                     Query Match
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ABM85149
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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp conclus may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline polymorphisms, as molecular weight markers, and for somatic or germline invention. Note: The sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gietzen D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosting a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Geretin BH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Ru Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gletzer
Patury S, Shi X, Suarez CJ;
                                                                                                                                                                                                                                                                                                                                                                                                gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
                                                             Gaps
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0
                                                                                                                                                                                                                                                                                                                                                         Human diagnostic and therapeutic pprotein SEQ ID NO:5399.
                                                           0; Indels
                    DB
9;
                                                           0; Mismatches
                      Score 41;
Pred. No.
                                                                                                                                                                                                                                       ABM85150 standard; protein; 455 AA.
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                    82.0%;
100.0%;
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12-SEP-2002; 2002US-0410260P.
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Query Match
Best Local Similarity luv...
7; Conservative
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45 GHRPLDK 51
                                                                                                  1 GHRPLDK 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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82.08;

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ABM85152 standard; protein; 474 AA
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12-SEP-2002; 2002US-0410260P.
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Best Local Similarity 100...
7; Conservative
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Kwong M,
Shi X,
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ABM6 5152

ADM 6152

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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be considered to diagnost a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp confections also be used in genetic mapping, in identifying individuals from minute biological samples in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline polymorphisms, as molecular weight markers a dithp protein of the invention. Note: The sequence represents a dithp protein of the invention, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
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UA, Kirton ES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Delegeane AM, Pensear IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang K, Au AP, Geretin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Ku Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietze
Patury S, Shi X, Suarez CJ;
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Length 474;
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DB 8;
9.4;
                        ilarity 100.0%; Pred. No. 9.4
Conservative 0; Mismatches
82.0%; Score 41;
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N-PSDB; ACN43130.
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                        Best Local Similarity
Matches 7; Conserv
                                                                                                     1 GHRPLDK 7
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  Query Match
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                                                                            Gaps
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                        8; Length 455;
                                                                            0; Indels
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                     82.0%; Score 41; DB
100.0%; Pred. No. 9;
ive 0; Mismatches
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DB 8; Length 474;

82.0%; Score 41;

Sequence 474 AA;

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Indels

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Mismatches

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Matches

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The invention relates to novel diagnostic and therapeutic polymucleotides selected from one of the 2722 sequences defined in the specification. A polymucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polymucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine with human molecules, e.g. cell proliferative disorders, endocrine disorder, neurological disorder, developmental disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp infections caused by virus, bacteria, fungi or parasite. The dithp conjuminate biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline polymorphisms, as molecular weight markers, and for somatic or germline invention. Note: The sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Harthshorne TA, Suchorolski MT, Altus CM, Pittes SJ, Elder LV;
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Stevens KA, Blanchard SR, Rioux P, Shen EJ, Wu MC, Stuve LL;
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Xu X, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
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                        Gaps
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SJ, Elder LV;
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                        0; Indels
100.0%; Pred. No. 9.4;
tive 0; Mismatches
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Best Local Similarity 100.
Matches 7; Conservative
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                                                          1 GHRPLDK 7
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                                                                                     GHRPLDK
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                                                                                                                                                       RESULT 37.
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DB 8; Length 474; 9.4;

Score 41; Pred. No.

82.0%; S 100.0%;

Query Match Best Local Similarity

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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, developmental disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp on molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline polymorphisms, as molecular weight markers, and for somatic or germline invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Harthdorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Lagace RB, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzer
Patury S, Shi X, Suarez CJ;
Gaps
                                                                                                                                                                                                                                                                                                                         gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
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                                                                                                                                                                                                                                                                                   Human diagnostic and therapeutic pprotein SEQ ID NO:4731.
                                                                                                                                                                    ABM84482 standard; protein; 474 AA.
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2002US-0410260P.
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Best Local Similarity
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12-SEP-2002;
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                                                                                                                                  RESULT 38
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The invention relates to novel diagnostic and therapeutic polymucleotides selected from one of the 2722 sequences defined in the specification. A profit of the invention may have a use in gene therapy. The human diagnostic and therapeutic polymucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine cutoimmune/inflammatory disorder, developmental disorders, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp conflections caused by virus, bacteria, fungi or parasite. The dithp conflections caused by virus, bacteria, fungi or parasite. The dithp crow minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline conflection. Note: The sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SY, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietze
                                                                                                                                                                                                                                                                                                          gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
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N-PSDB; ACN43803.
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45 GHRPLDK 51
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S, Shi X,
GHRPLDK
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The invention relates to a composition comprising several CDNAs that are differentially expressed in a liver disorder. The composition is useful to the treating liver disorder such as hyperlipidaemia, hyperension, type II diabetes, tumnours of the liver and disorders of the inflammatory and immune response. The composition is useful for a high-throughput method of several molecules or compounds to identify a ligand which specifically binds a cDNA. A protein encoded by the cDNA is useful for a high-throughput method for using a protein to screen several molecules or compounds to identify at least one ligand which specifically binds the protein which involves combining the protein encoded by the cDNA with several of molecules or compounds under conditions to allow specific or binding, and detecting specific binding between the protein and a molecule or compound, therefore identifying a ligand which specifically binds the protein. The composition is useful for detecting and conditions is useful for detecting and composition is useful for detecting and composition is useful for detecting and committed formulate prognosis and to design a treatment regimen and to monitor the efficacy of treatment. The present sequence represents the amino acid sequence of a protein encoded by a cDNA differentially expressed in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition comprising several cDNAs that are differentially expressed in treated human C3A liver cell cultures, useful for treating liver
                                                                                                                                                       human; liver disorder; hyperlipidaemia; hypertension; type II diabetes; tumour; liver; inflammatory disorder; immune response disorder; high-throughput screening; differential gene expression; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                  Human protein expressed in a liver disorder #11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 33; 41pp; English
ADE76868 standard; protein; 488 AA.
                                                                                                                                                                                                                                                                                                                                                         30-JUL-2001; 2001US-00919039.
                                                                                                                                                                                                                                                                                                                                                                                              28-JUL-2000; 2000US-0222113P.
                                                                             29-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100...
7; Conservative
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N-PSDB; ADE76867.
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                                                                                                                                                                                                                                       sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders.
                                    ADE76868;
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82.0%; Score 41; DB 8; Length 474; 100.0%; Pred. No. 9.4; rive 0; Mismatches 0; Indels

Best Local Similarity 100. Matches 7; Conservative

Query Match

Sequence 474 AA;

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Sequence 11, Appl Sequence 10, Appl Sequence 6, Appl Sequence 12, Appl Sequence 12, Appl Sequence 10, 
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                                                                                                    June 1, 2005, 11:41:40; Search time 32 Seconds (without alignments) 18.662 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 33
Sequence 4,
Sequence 96
Sequence 18
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Sequence
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Sequence
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  /cgn2 6/ptodata1/iaa/5A_COMB.pep:*
  /cgn2 6/ptodata1/liaa/5B_COMB.pep:*
  /cgn2 6/ptodata1/liaa/6A_COMB.pep:*
  /cgn2 6/ptodata1/liaa/6B_COMB.pep:*
  /cgn2 6/ptodata1/liaa/PCTUS COMB.pep:*
  /cgn2 6/ptodata1/liaa/PCTUS COMB.pep:*
  /cgn2 6/ptodata1/liaa/backfiles1.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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.09-252-991A-18909
.09-252-991A-18782
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-09-513-999C-4232
-09-513-999C-4231
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                                                                                                                                                                                                                                                                                                            513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                       - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                    US-09-424-940A-2
50
1 GHRPLDKC R
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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                                                                                                                                                                                                                     Sequence:
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                                                                                                         Run on:
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No.
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e 26425, A e 21990, A e 21990, A e 39157, A e 54374, App e 234, App e 234, App e 16727, A e 38, App e 38, Appl e 38, Appl e 38, Appl			Gaps (
Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seq			,
28 36 72.0 74 4 US-09-248-796A-26425 SS 29 36 72.0 194 4 US-09-252-991A-21350 SS 31 35 72.0 194 4 US-09-252-991A-21990 SS 31 35 70.0 155 4 US-09-270-767-39157 SS 32 70.0 1203 4 US-09-799-875-5 33 35 70.0 1203 4 US-09-799-875-5 34 68.0 9 3 US-09-042-1170-234 SS 34 68.0 9 4 US-09-72-250D-234 SS 34 68.0 9 4 US-09-676-475A-234 SS 34 68.0 9 4 US-09-676-475A-234 SS 34 68.0 245 4 US-09-676-475A-234 SS 34 68.0 245 4 US-09-676-475A-234 SS 34 68.0 245 4 US-09-676-475A-38 SS 46.0 245 4 US-08-466-38 SS 47 68.0 378 4 US-08-373-902-1 SS 47 68.0 378 4 US-08-373-902-1	ALIGNMENTS	RESULT 1 US-08-059-11 Sequence 11, Application US/08058699 Fatent No. 544387 Patent No. 544387 FERENAL INFORMATION: APPLICANT: Edgar Haber APPLICANT: Christoph Bode APPLICANT: Marschall S. Runge TITLE OF INVENTION: THROWEIN NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: CONFUREY: Massachusetts COUNTRY: U.S.A. ZIP: 02110-2804 CONFURER: Massachusetts COMPUTER: IM PSS/2 Model 502 or 558X ODERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: Worderfect (Version 5.1) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/058,699 FILING DATE: 19330503 CLASSIPICATION NUMBER: US/08/058,699 FILING DATE: N/A APPLICATION NUMBER: 34 819 REFERENCE/DOCKET NUMBER: 0433/004001 TELEPHONE: (617) 542-5070 TELEPHONE: (617) 542-5070 TELEPHONE: (617) 542-5070 TELEPHONE: (617) 542-5070 TELERA: 200154 TELERA: AMINO ACID TELEMOTH: MANDO ACID TELEMOTH: MANDO ACID TTELEMOTH: MANDO ACID	Query Match 100.0%; Score 50; DB 1; Length 8 Best Local Similarity 100.0%; Pred. No. 4.1e+05; Matches 8; Conservative 0; Mismatches 0; Indels

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US-10-142-935-6

Sequence 6, Application US/10142935

Patent No. 6835-70

Patent No. 6835-70

Patent No. 6835-70

APPLICANT: DAVIS, Stacey

APPLICANT: DAVIS, Stacey

ITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATIC

FILE REFERENCE: PO7201US01/BAS

CURRENT APPLICATION NUMBER: US/10/142,935

CURRENT APPLICATION NUMBER: US 60/290,072

PRIOR FILING DATE: 2001-05-13

PRIOR FILING DATE: 2001-05-13

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PatentIn version 3.1

SEQ ID NO 6

LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 10;
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                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,547
FILING DATE: 30-JUN-1995
FILOR APPLICATION 1435
PRIOR APPLICATION NUMBER: PCT/JP94/01844
FILING DATE: 01-NOV-1994
PRIOR APPLICATION NUMBER: DF 5-297325
FILING DATE: 02-NOV-1993
ATPONEY/AGENT NFORMATION:
AND APPLICATION PATA:
ATPLICATION NUMBER: DF 5-297325
FILING DATE: 02-NOV-1993
ATPONEY/AGENT NFORMATION:
    ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0-38931
                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: Q-31
TELEPHONE: (202)293-7060
TELEPHONE: (202)293-7060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.0%; £
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Conservative
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MOLECULE TYPE: peptide
                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-448-547-1
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US-08-448-547-1
; Sequence 1, Application US/08448547
; Patent No. 5821068
; GENERAL INFORMATION:
APPLICANT: Soe, Gilbu
; APPLICANT: Kohno, Isao
; APPLICANT: Inzuka, Kimiko
; APPLICANT: Ito, Yumiko
; TITLE OF INVENTION: ANTI-HUMAN SOLUBLE FIBRIN ANTIBODY,
; TITLE OF INVENTION: HYBRIDOMA, AND IMMUNOASSAYING METHOD
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 7;
                                                                                                                                                                                                                        APPLICANT: Christoph Bode
APPLICANT: Ragar Haber
APPLICANT: Bagar Haber
APPLICANT: Bagar Haber
APPLICANT: Bagar Haber
APPLICANT: Marschall S. Runge
TITLE OF INVENTION: THROMBIN
NUMBER OF SEQUENCES: 12
COMBESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STREET: 225 Franklin Street
CITY: Boston
STREET: 3.5 Franklin Street
CITY: Boston
STREET: 3.5 Franklin Street
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER RADABLE FORM:
MEDIUM TYPE: 3.5 Diskette, 1.44 Mb
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Diskette, 1.44 Mb
COMPUTER RADABLE FORM:
MEDIUM TYPE: 3.5 DISKETTE, 1.0
CONTRY: WordPerfect (Version S.0)
SOFTWARE: WordPerfect (Version S.1)
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/058,699
FILING DATE: 19930503
CIASSIFICATION DATA:
APPLICATION NUMBER: N/A
ATTORNEY/AGENT INFORMATION:
NAME: Janis K. Fraser, Ph.D.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/004001
TELEPHONE: (617) 542-5070
TELEFRAX: (617) 542-5070
TELEFRAX: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.1e+05;
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                                                                                                                                                           ; Sequence 10, Application US/08058699; Patent No. 5443827; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELERAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 82.0
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: Linear
US-08-058-699-10
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US-08-058-699-10
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APPLICANT: Buttram, Scott
APPLICANT: McBride, William
APPLICANT: Lister-James, John
APPLICANT: Lister-James, John
APPLICANT: Civitello, Edgar R
TITLE OF INVENTION: Technetium-99m Labeled Peptides for
TITLE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
COTTY: Chicago
                                                                                                                                                             Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.0%; Score 41; DB 1; Length 28; 100.0%; Pred. No. 0.32; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,152
FILING DATE: 06-JUN-1995
CLASSIPICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: NO. 5780007nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,205-L
TELECHOWINICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/08468964B; Patent No. 5922303; GENERAL INFORMATION:
                                                                                                                                   82.0%; Sc.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-470-152-12; Sequence 12, Application US/08470152; Patent No. 5780007; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                          Conservative
                         ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-486-135-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                          Query Match
Best Local Similarity
''^a 7; Conserva
      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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1 GHRPLDK 7
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                                                                                                                                                                                                                                                                                 GHRPLDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-468-964B-10
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                                                                                                          US-10-142-935-4
Sequence 4, Application US/10142935
GENERAL INFORMATION:
MAGNUS A.O.
TITLE DE INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATI
FILE REFERENCE: PO7201US01/BAS
CURRENT APPLICATION NUMBER: US/10/142,935
CURRENT FILING DATE: 2002-05-13
PRIOR FILING DATE: 2001-05-13
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 4
IENGTH: 25
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| Patent No. 5720934
| GENERAL INFORMATION:
| APPLICANT: Dean, Richard T
| APPLICANT: Dean, Scott
| APPLICANT: Butram, Scott
| APPLICANT: Lister-James, John
| APPLICANT: Lister-James, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.0%; Score 41; DB 4; Length 25; 100.0%; Pred. No. 0.29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
SOFTWARE Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,135
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 5720934nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,205-N
TELECOMMUNICATION INFORMATION:
TELEPOMN: 312-715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Preu. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 amino acide
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10 GHRPLDK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 GHRPLDK 21
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Matches 7; Conserv
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US-08-486-135-12
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Patent No. 598519
GENERAL INFORMATION:
APPLICANT: Dean, Richard T
APPLICANT: Dean, Richard T
TITLE OF INVENTION: Technetium-99m Labeled Peptides for TITLE OF INVENTION: Taging Inflammation
NUMBER OF SEQUENCE: 37
CORRESPONDENCE ADDRESS:
ADDRESSEB: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STRATE: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STRATE: 111inois
COUNTRY: USA
ZIP: 60606
COMPUTER RADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC Compatible
OPERATING SYSTEM: PC Compatible
COMPUTER: DestentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,853
FILING DATE: 11-OCT-1994
CLASSIFICATION NUMBER: 92,112-H
REGISTRATION NUMBER: 92,112-H
TELEPHONE: 312-715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.0%; Score 41; DB 2; Length 28; 100.0%; Pred. No. 0.32;
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION VINSER: US/07/871,282A
FILING DATE: 20-APP-1992
                                                                                                                                                    CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MCDAniels, Patricia A.
REGISTRATION NUMBER: 33,194
REFERENCE/DOCKET NUMBER: DITI 111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (603) 437-8970
TELEPHONE: (603) 437-8970
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: not rele
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GHRPLDK 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-07-871-282A-10
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                    APPLICANT: Butrram, Scott
APPLICANT: Butrram, Scott
APPLICANT: McBride, William
APPLICANT: Lister-James, John
APPLICANT: Civitello, Edgar R.
TITLE OF INVENTION: Technetium-99m Labeled Peptides for
TITLE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Diatide, Inc.
STREET: 9 Delta Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Dean, Richard T.
APPLICANT: Buttram, Scott
APPLICANT: Buttram, Scott
APPLICANT: Lister-James, John
APPLICANT: Joh
APPLICANT: John
APPLICANT: John
APPLICANT: John
APPLICANT: John

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 03053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,964B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MCDENIELS. Patricia A.
REGISTRATION NUMBER: 33,194
REGISTRATION NUMBER: 33,194
REGISTRATION NUMBER: 31,194
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Pred. No.
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Patent No. 5965107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: not relevant
Dean, Richard T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 82.0
Best Local Similarity 100.
Matches 7; Conservative
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US-07-871-282A-10
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1 GHRPLDK 7
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1 GHRPLDK 7
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                                                                                                                               /label= Amide
/note= "The carboxyl terminus is modified to an amide"
  /label= BAT /note= "The amino terminus is linked to a BAT radiolabel binding moiety."
                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                        82.0%; Score 41; DB 2; Length 28;
100.0%; Pred. No. 0.32;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/08253678A

Parent No. 599784

GENERAL INFORMATION:
APPLICANT: Buttram, Scott
APPLICANT: Lister-James, John
APPLICANT: Lister-James, John
APPLICANT: Civitello, Edgar R.
TITLE OF INVENTION: TECHNETIUM-99m LABELED PEPTIDES FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.0%; Score 41; DB 2; Length 28; 100.0%; Pred. No. 0.32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA

ZIP: 03053

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/253,678A
FILING DATE: 03-UW-1994
ATTOREY APELICATION: 424
ATTOREY AGENT INFORMATION:
ANDRE: MCDENSIFICATION: 1800MATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Pred. No. 0.3
:ive 0; Mismatches
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STRANDEDNESS: not relevant
                                                            FEATURE:

NAME/KEY: Modified-site

LOCATION: 28

OTHER INFORMATION: /label-
OTHER INFORMATION: /note=

OTHER INFORMATION: amide"
US-08-290-853-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Diatide, Inc.
STREET: 9 Delta Drive
                                                                                                                                                                                                                                      Query Match 82.0
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Londonderry
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US-08-253-678A-10
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US-68-2144-10. Application US/0858134B

Partent No. 607427

(GRREAL INCOMATION

APPLICATY: MELICAM SILIS

APPLICATY: MACING

CONTENT OF INVERTION: IMMCING

CONTENT: MISS

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us-09-424-940a-2.rai

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/label= Amide
/note= "The carboxyl terminus is modified to an
amide"
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0
                                                                                                                                                                                                                                           /note= "The amino terminal residue is
pyridine-2-carbonyl; the thiol of the
protected by an acetamidomethyl group.
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OTHER INFORMATION: /label= Picolinoyl
OTHER INFORMATION: /note= "The amino terminal residue is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Dean, Richard T
APPLICANT: Lees, Robert S.
APPLICANT: Buttram, Scott
TITLE OF INVENTION: Technetium-99m Labeled Peptides for TITLE OF INVENTION: Imaging Inflammation
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
ATONENY AGENT INPORMATION:
NAME:
ATONENY AGENT INPORMATION:
NAME:
ATONENY AGENT INPORMATION:
TELEPRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 35,303
TELEFRAX: 312-715-1204
TELEFRAX: 312-715-1204
TELEFRAX: 312-715-1204
TELEFRAX: 312-715-1317
INPORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STAFE: 111inois
COUNTR: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CONPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.0%; Score 41; DB 100.0%; Pred. No. 0.3 iive 0; Mismatches
                                                                                                                                         NAME/KEY: Modified-site
LOCATION: 1.3
LOCATION: 1.3
COTHER INPORMATION: /label= Picolinoyl
OTHER INFORMATION: pyridine-2-carbonyl;
OTHER INFORMATION: pyridine-2-carbonyl;
FEATURE:
NAME/KEY: Modified-site
LOCATION: 30
OTHER INFORMATION: /label= Amide
OTHER INFORMATION: /label= Amide
OTHER INFORMATION: /note= "The carboxyl
OTHER INFORMATION: amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/08472535 Patent No. 5711931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.'
Matches 7; Conservative
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GHRPLDK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GHRPLDK 7
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; Sequence 35, Application US/08290853
; Patent No. 5080519
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for TITLE OF INVENTION: Imaging Inflammation
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for TITLE OF INVENTION: Imaging Inflammation
; TITLE OF INVENTION: Imaging Inflammation
; VITLE OF INVENTION: Imaging Inflammation
; VITLE OF INVENTION: Imaging Inflammation
; VITLE OF INVENTION: Allegretti, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; CONPOTER: Illinois
; COMPUTER READABLE FORM:
; GONFORTER: PROPY disk
; COMPUTER: PRECHIN Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/20,853
; FILING DATE: 11-OCT-1994
; TILING DATE: 11-OCT-1994
; ATTOANEY ASTERNI FORMER: ATTOANEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.0%; Score 41; DB 3; Length 28; 100.0%; Pred. No. 0.32; tive 0; Mismatches 0; Indels
                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/170,299
FILING DATE: 09-FEB-1995
                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
ATYORNEY/AGENT INFORMATION:
NAME: No. 5989519nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,112-H
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TELEPHONE: 312-715-1000
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TELEX: 910-221-5317
INPORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 7; Conservative
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US-08-290-853-35
                          COUNTRY:
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US-08-266-178A-9
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; OTHER INFORMATION: pyridine-2-carbonyl; the thiol of the cysteine; OTHER INFORMATION: residue is protected by an acetoamidomethyl US-08-472-535-9
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OTHER INFORMATION: /label= Picolinoyl
OTHER INFORMATION: /note= "The amino terminal residue is
OTHER INFORMATION: pridine-2-carbonyl; the thiol of the cysteine
OTHER INFORMATION: residue is protected by an acetoamidomethyl
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US-08-484-774-9
; Sequence 9, Application US/08484774
; Patent No. 5807538
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
APPLICANT: Lees, Robert S.
; APPLICANT: Buttram, Scott
; TITLE OF INVENTION: Imaging Inflammation
; TITLE OF INVENTION: Imaging Inflammation
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.0%; Score 41; DB 1; Length 31;
100.0%; Pred. No. 0.36;
ive 0; Mismatches 0; Indels
                                                                                                                                                                     82.0%; Score 41; DB 1; Length 31;
100.0%; Pred. No. 0.36;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy 
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TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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TOPOLOGY: linear
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4 GHRPLDK 10
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Sequence 4232, Application US/09513999C
| Patent No. 6783961|
| GENERAL INFORMATION:
| APPLICANT: Dumas Milne Edwards, J.B.
| APPLICANT: Duclett, A.
| APPLICANT: Duclett, A.
| APPLICANT: Giordano, J.Y.
| TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
| PILE REPERENCE: 59.US.RED
| CURRENT APPLICATION NUMBER: US/09/513,999C
| CURRENT PLING DATE: 1999-02-26
| PRIOR APPLICATION NUMBER: US 60/122,487
| RING RELIGIOR DATE: 1999-02-26
| NUMBER OF SEQ ID NOS: 36681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COCATION: 1...3

OTHER INFORMATION: /label= Picolinoyl
OTHER INFORMATION: /note= "The amino terminal residue is
OTHER INFORMATION: /note= "Teamino terminal residue is
OTHER INFORMATION: pytidine-2-carbonyl; the thiol of the cysteine
OTHER INFORMATION: residue is protected by an acetoamidomethyl
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Sequence 9, Application US/08266178A
Parent No. 6017510
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Technetium-99m Labeled Peptides for TITLE OF INVENTION: Technetium-99m Labeled Peptides for TITLE OF INVENTION: Imaging Inflammation
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: 10 South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.0%; Score 41; DB 3; Length 31;
100.0%; Pred. No. 0.36;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILLING DATE: 27-JUN-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: NO. 6017510nan, Kevin B
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,112
TELECOMUNICATION INFORMATION:
TELEBHONE: 312-115-1000
TELEFAX: 312-715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELERAX: 312-/15 TELEX: 910-221-5317
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Modified-site
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Best Local Similarity luv...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                       STREET: 10 South
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 GHRPLDK 10
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RESULT 17

Gaps

; 0

0; Indels

DB 4; Length 488; 5.8;

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TYPE: PRT
CRGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
CTHER INFORMATION: Incyte ID No. 6727066 3393861CD1
US-09-919-039-33
                                                                                                                                                                       Query Match
82.0%; Score 41; DB
Best Local Similarity 100.0%; Pred. No. 5.8
Matches 7; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Parker, Gary E
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-08-206-176-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                  42 CHRPLDK 48
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US-09-949-016-9617
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US-08-206-176-4
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US-09-919-039-33
US-09-919-039-33
Sequence 33, Application US/09919039
Patent No. 6727066
GENERAL INFORMATION:
APPLICANT: Kaser, Matthew R.
TITLE OF INVENION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT APPLICATION NUMBER: US/09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR PILING DATE: 2000-07-28
NUMBER: OF SEQ ID NOS: 401
SOFTWARE: PERL PROGram
SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 19
US-09-513-999C-4231
; Sequence 4231. Application US/09513999C
; Patent No. 678361.
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Dioclert, A.
; APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 678361.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT APPLICATION NUMBER: US/09/512,487
; PRIOR APPLICATION NUMBER: US/06/122,487
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4231
LENGTH: 150
; TYPE: PRT
ORGANISM: Homo sapiens.
                                                                                                                                                                                                                                                                                                    Gaps
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0
                                                                                                                                                                                                                                                     Query Match
82.0%; Score 41; DB 4; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches, 7; Conservative 0; Mismatches 0; Indels
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Matches 7; Conservative 0; Mismatches
                                                                                                                                               LOCATION: -30..-1
COTHER INFORMATION: SCORE 12.2
CHER INFORMATION: SEG LLLLLLCVFLVKS/QG
US-09-513-99QC-4232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: SCORE 12.2
; OTHER INFORMATION: SEQ LLLLLLCVFLVKS/QG
US-09-513-999C-4231
                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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45 GHRPLDK 51
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SOFTWARE: Patent.pm
SEQ ID NO 4232
LENGTH: 118
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                                                                                                                             NAME/KEY: SIGNAL
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                                                                   APPLICANT: Garner, Ian
APPLICANT: Garner, Ian
APPLICANT: Dalrymple, Michael A
APPLICANT: Prunkard, Donna E
APPLICANT: Foster, Donnald C
TITLE OF INVENTION: Production of Fibrinogen in Transgenic
TITLE OF INVENTION: Animals
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.0%; Score 41; DB 1; Length 491;
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                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/206,176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 82.0%; Score 41; up 1; Best Local Similarity 100.0%; Pred. No. 5.8; Matches 7; Conservative 0; Mismatches
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Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPERRICE/DOCKET NUMBER: 31-648
REPERRICE/DOCKET NUMBER: 93-15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
PURILEPRI: 206-548-9190
                                                                                                                                                                                                                                                                    ADDRESSEB: ZymoGenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
Sequence 4, Application US/08206176
Patent No. 5639940
GENERAL INFORMATION:
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Securice 9.9, Application US/10142935

Setting 2017

FILE REFERENCE: P07201US01/BAS

CURRENT FILING DATE: 2002-05-13

FRIOR PAPLICATION NUMBER: US/10/142,935

CURRENT FILING DATE: 2001-05-13

FRIOR PAPLICATION NUMBER: US 60/290,072

FRIOR PAPLICATION NUMBER: US 60/290,072

FRIOR PAPLICATION NUMBER: US 60/290,072

FRIOR FILING DATE: 2001-05-13

SUPPRESE PARCHING PAPLE: 2001-05-13

SUPPRESE PARCHING PAPLE: 100

LENGTH: 10
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Parent No. 6835378
GENERAL INFORMATION
APPLICANT: DAVIS, Stacey
APPLICANT: HOOK, Magnus A.O.
TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATI
FILE REFERENCE: P07201US01/BAS
CURRENT APPLICATION NUMBER: US/10/142,935
CURRENT APPLICATION NUMBER: US/002010513
FRIOR APPLICATION NUMBER: US 60/290,072
PRIOR FILING DATE: 2001-05-13
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Pred. No. 12;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18782
LENGTH: 177
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                                                                                                                                                                  ORGANISM: Pseudomonas aeruginosa
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SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 15
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17 GHRPIARC 24
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Matches 6; Conserv
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Matches 5; Conser
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US-10-142-935-8
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US-10-142-935-8
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APPLICANT:
MAIC J. Rubenfield et al.

APPLICANT:
MAIC J. Rubenfield et al.

TITLE OF INVENTION:
TITLE OF INVENTION:
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION:
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION:
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER: OS 60/094,190
RION FILING DATE: 1998-07-27
SEQ ID NOS: 33142
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APPLICANT: MATC J. RUBERFIELD & A. J.
APPLICANT: MATC J. RUBERFIELD AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT PELLING NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
              APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLOOL307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-30

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-08

PRIOR PILING DATE: 2000-10-09

PRIOR PILING DATE: 2000-10-09

PRIOR PILING DATE: 2000-10-08

NUMBER: OF SEQ ID NOS: 207012

SOPTWARE: PSELSEQ for Windows Version 4.0

SEQ ID NO 9617
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Pred. No. 6.7;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) ORGANISM: Pseudomonas aeruginosa US-09-252-991A-18909
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85.7%;
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US-09-252-991A-18909
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US-09-252-991A-18782
                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-949-016-9617
                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REPERENCE: 107196.136 CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR PAPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-02-18 PRIOR FILING DATE: 1998-02-7 NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 23750 LENGTH: 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196_136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER: OF SEQ ID NOS: 33142
SEQ ID NO 2 1990
LENGTH: 246
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Patent No. 6703491
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 39157
LENGTH: 1555
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21;
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Pred. No. 34;
1; Mismatches
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ORGANISM: Drosophila melanogaster
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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77.8%;
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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US-09-252-991A-21990
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                                                                                                                                                                 Sequence 5, Application US/10142935
Patent No. 683378
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DAVIS, Stacey
APPLICANT: HOOK, Magnus A.O.
TITILE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROWBIN-INDUCED COAGULATI
TITILE OF INVENTION NUMBER: US/10/142,935
CURRENT APPLICATION NUMBER: US 60/290,072
PRIOR PELING DATE: 2001-05-13
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
SEQ ID NO 5.
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US-09-248-796A-26425
US-09-248-796A-26425
Sequence 26425. Application US/09248796A
Facent No. 6747137
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN TITLE OF INVENTION: NUMBER: US/09/248,796A
TITLE OF INVENTION: NUMBER: US/09/248,796A
CURRENT APPLICATION NUMBER: US 60/074,725
FRIOR PILING DATE: 1998-02-13
FRIOR FILING DATE: 1998-08-13
FRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
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Pred. No. 8;
0; Mismatches
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US-09-252-91A-23750
; Sequence 23750, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.0%;
85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 6; Conservative
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                                                                  10 GHRPLD 15
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15 GHRPLD 20
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Best Local Similarity
Matches 6; Conserv
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                         GHRPLD 6
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LENGTH: 74
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US-10-142-935-5
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4 RPIDKC 9
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4 RPIDKC 9
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US-09-722-250D-234
                                      RESULT 34
US-09-258-754-234
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US-09-270-767-54374
US-09-270-767-54374

Sequence 54374, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster:
FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DARE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 54374
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Sequence 5, Application US/09799875
Sequence 5. Application US/09799875
Sexent No. 6638721
Sexent INPORMATION:
APPLICANT: Mayers, Rachel
APPLICANT: Williamson, Mark
TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses
TITLE OF INVENTION: Therefor
FILE REPERENCE: 35800/20996
CURRENT APPLICATION NUMBER: 08/09/799,875
CURRENT FILING DATE: 2000-03-06
PRIOR PILING DATE: 2000-02-11
PRIOR PILING DATE: 2000-09-12
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 1203
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Pred. No. 2.1e+02;
0; Mismatches 1; Indels
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                                                     70.0%; Score 35; DB 4; Length 155; 71.4%; Pred. No. 26; ive 1; Mismatches 1; Indels
; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-39157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Xaa means any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 155
TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.0%;
                                                                      Best Local Similarity 71.4
Matches 5; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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US-09-799-875-5
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6 HRPIDLC 12
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6 HRPIDLC 12
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US-09-799-875-5
                                                     Query Match
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Sequence 234, Application US/09258754
; Sequence 234, Application US/09258754
; Sequence 234, Application US/09258754
; Beant No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REPRENCE: P-LJ 3443
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; RARLIER PILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 234

LENGTH: 9
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APPLICANT: Rucelahti, Renata
TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
TITLE OF INVENTION: Tissues
FILE REFERENCE: P-LJ 2892
CURRENT APPLICATION NUMBER: US/09/042,107
CURRENT FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 436
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 9;
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Pred. No. 4.1e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-042-107-234
; Sequence 234, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.0%;
83.3%;
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Best Local Similarity 83.3.
اتمام 5، Conservative
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Gaps
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APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BULJUK
APPLICANT: ISA K. MUSHAHWAR
APPLICANT: ISA K. MUSHAHWAR
APPLICANT: ISA K. MUSHAHWAR
APPLICANT: ISA K. MUSHAHWAR
TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
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                                                                                                                                                                                                                                          Length 190;
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                                                                                                                                                                                                                                                                                       1; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,260A
                                                                                                                                                                                                                                        Score 34; DB 4;
Pred. No. 51;
1; Mismatches
           PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 16727
LENGTH: 190
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOHN N. SIMONS
TAMI J. PILOT-MATIAS
GERORGE J. DAMSON
GEORGE G. SCHLAUDER
SURESH M. DESAI
THOMAS P. LEARY
ANTHONY SCOTT MUERHOFF
JAMES C. ERKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 38, Application US/08469260A
Patent No. 6451578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
                                                                                                                                                                                                                                          68.0%;
71.4%;
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 245 amino acids
                                                                                                                                                                       ; ORGANISM: Candida albicans
US-09-248-796A-16727
                                                                                                                                                                                                                                      Query Match
Best Local Similarity 71.4
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                          109 HRPIDIC 115
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APPLICANT: JOHN N
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Patent No. 6747137

REBERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN FILLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILLE REPERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
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APPLICANT: Ruoslahti, Renata
APPLICANT: Ruoslahti, Renata
APPLICANT: Rajotte, Danial
APPLICANT: Rajotte, Danial
TITLE OF INVENTION: Membrane Dipeptidase
TITLE OF INVENTION: Membrane Dipeptidase
FILE REFERENCE: P-LA 4377;
CURRENT APPLICATION NUMBER: U$/09/676,475A
CURRENT FILING DATE: 1998-03-13
FRIOR APPLICATION NUMBER: 09/042,107
PRIOR APPLICATION NUMBER: 09/042,107
PRIOR PILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 452
SOFTHARE: Patentin Ver. 2.0
SSEQ ID NO 234
LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
TITLE OF INVENTION: Tissues
FILE REPERRATION: Tissues
FILE REPERRACE: P.1.4 4514
CURRENT FILING DATE: 2000-11-22
PRIOR PILING DATE: 1998-0313
NUMBER OF SEQ ID NOS: 437
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 234
LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-676-475A-234
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Pred. No. 4.1e+05;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 234, Application US/09676475A; Patent No. 6784153; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  68.0%;
83.3%;
                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 83.3
Matches 5; Conservative
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RPIDKC 9
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4 RPIDKC 9
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US-09-248-796A-16727
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US-09-676-475A-234
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                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: TRAIL JOHN SINGNS
APPLICANT: TRAIL JOHN SINGNS
APPLICANT: GEORGE G SCHLAUDER
APPLICANT: GEORGE G SCHLAUDER
APPLICANT: GEORGE G SCHLAUDER
APPLICANT: THOMAS COUT MURRHOFF
APPLICANT: THOMAS C. ERKER
APPLICANT: THOMAS C. ERKER
APPLICANT: SHERI L. BILJAK
APPLICANT: JANGON SCOTT MURSHOFF
APPLICANT: JANGON SINGNS
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: ADDRESSE: ADDRESSEE: ABBOTT PARK ROAD
CITY: ABBOTT PARK ROAD
CITY: ABBOTT PARK ROAD
CITY: ABBOTT PARK
COUNTRY: USA
COUNTRY: USA
COMPUTER: IBM PC COMPATIBLE FORM:
MEDIUM TYEB: PLOPPY disk
COUNTRY: USA
COMPUTER: PATENDALE FORM:
MEDIUM TYEB: PLOPPY disk
COUNTRY: ABBOTT PARK
MEDIUM TYEB: PLOPPY disk
COMPUTER: PATENDALE FORM:
MEDIUM TYEB: PLOPPY DISK
COMPUTER: NON-EHEAGE FORM:
MEDIUM TYEB: PLOPPY DISK
COMPUTER: NON-EHEAGE FORM:
MEDIUM TYEB: PLOPPY DISK
COMPUTER: PATENDALE:
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MEDIUM TYER: PLOPPY DISK
COMPUTER: PATENDALE:
MEDIUM TYER: PLOPPY DISK
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                                 2; Indels 0;
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Best Local Similarity 75.0%; Pred. No. 65; Matches 6; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                 Sequence 38, Application US/08488446
Patent No. 6558898
GENERAL INPORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: TAMI J. PILOT-MATIAS
APPLICANT: GEORGE J. DAWSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
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                                                                                                                                      1 | | | | | | | 25 GRRPLAKC 32
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Best Local Similarity
Matches 6; Conserva
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Search completed: June 1, 2005, 11:53:57 Job time: 33 secs

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Sequence 42547, A Sequence 29, Appl Sequence 18735, Sequence 128550, Sequence 187347, Sequence 187347, Sequence 6311, Ap Sequence 9, Appli Sequence 9, Appli

6831, Ap 9, Appli 8, Appli 7, Appli 5, Appli 132166,

Sequence 7 Sequence 5 Sequence 1

us-09-424-940a-2.rapb

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Sequence 6, Application US/10450073
; Sequence 6, Application US/10450073
; Publication No. US2004013296941
; GENERAL INFORMATION:
    APPLICANT: Melvin, William T
; APPLICANT: Thompson, William D
; APPLICANT: Thompson, William D
; APPLICANT: Thirstina M
; TITLE OP INVENTION: Antibodies, Peptides, Analogs and Uses Thereof
; FILE REFERENCE: 0380-P02213050
; CURRENT APPLICATION NUMBER: US/10/450,073
; CURRENT FILING DATE: 2003-06-09
; PRIOR FILING DATE: 2001-12-12
; PRIOR PELING DATE: 2000-12-12
; PRIOR PELING DATE: 2000-12-12
; RIOR APPLICATION NUMBER: GB 0030309.9
; PROFINENCE DATE: 2000-12-12
; SEQ ID NOS: 9
; SEQ ID NO 6
; LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: Synthesised US-10-450-073-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 14;
US-10-425-114-42547
US-10-436-198-29
US-10-437-963-12855
US-10-437-963-12855
US-10-437-963-12855
US-10-437-963-187113
US-10-437-963-187113
US-10-437-963-187113
US-10-437-963-187113
US-10-437-963-132166
US-10-142-935-8
US-10-142-935-8
US-10-142-935-8
US-10-142-935-8
US-10-142-935-8
US-10-142-935-8
US-10-142-935-8
US-10-142-935-8
US-10-1437-963-13267
US-10-437-963-12867
US-10-437-963-128996
US-10-437-963-148999
US-10-437-963-148999
US-10-437-963-148999
US-10-437-963-148999
US-10-437-963-148999
US-10-437-963-148999
US-10-017-161-468
US-10-017-161-25-67-61
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   1 GHRPLDK 7
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GHRPLDK 7
 RESULT 1
US-10-450-073-6
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Sequence 294, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 1709, Ap
Sequence 33, Appli
Sequence 7552, Ap
Sequence 7552, Ap
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Sequence 6, Appli
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                                                                                                                      June 1, 2005, 11:44:05; Search time 99.7333 Seconds (without alignments) 27.728 Million cell updates/sec
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1: \cgn2 \( \) \cgn \( \) 
               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-864-408A-7552
US-10-437-963-114771
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US-10-142-935-6
US-10-142-935-6
US-10-459-030B-294
US-10-131-543-5
US-10-131-546-5
US-10-131-346-5
US-10-415-024-5
US-10-415-024-5
US-10-276-774-1709
US-10-919-039-33
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Sequence 127165, Sequence 127165, Sequence 12627, A Sequence 114710, Sequence 118819, Sequence 129796, Sequence 129796, Sequence 468, App Sequence 468, App Sequence 468, App Sequence 404, App Sequence 418, App

Sequence 2, Appli Sequence 259761, Sequence 156, App

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TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY
TITLE OF INVENTION: CHROMANS
FILE REFERENCE: 09744-018001
CURRENT APPLICATION NUMBER: US/10/131,546
CURRENT FILING DATE: 2002-04-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5. Application US/10131543

Publication No. US20030072709A1

GENERAL INFORMATION:

APPLICANT: Cyr. John E.

APPLICANT: Pearson, Daniel A.

TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS

TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL

CURRENT APPLICATION NUMBER: US/10/131,543

CURRENT PEPLICATION NUMBER: US/10/131,543

CURRENT PEPLICATION NUMBER: US/09/694,992

PRIOR FILING DATE: 2000-10-24

PRIOR FILING DATE: 2000-10-24

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PABLICATION NUMBER: PCT/US01/50423

SOFTWARE: PABLICATION NUMBER: US/09/694,992

SOFTWARE: PABLICATION NUMBER: US/09/694,992

SOFTWARE: PABLICATION NUMBER: US/09/694,992
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                                                                                                                                                                                                                                   82.0%; Score 41; DB 16;
100.0%; Pred. No. 1.6;
tive 0; Mismatches 0
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NUMBER OF SEQ ID NOS: 296
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 294
LENGTH: 28
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PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: PCT/US01/50423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Synthetic construct
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Publication No. US20030103895A1
GENERAL INFORMATION:
APPLICANT: Cyr, John E.
APPLICANT: Pearson, Daniel A.
                                                                                                                                                           ; OTHER INFORMATION: peptide Bbeta
US-10-459-030B-294
                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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4 GHRPLDK 10
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US-10-131-543-5
                                                                                                                                          FEATURE:
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    Sequence 6, Application US/10142935
Publication No. US20030044418A1
Sequence 6, Application US/10142935
Publication No. US20030044418A1
APPLICANT: INFORMATION:
APPLICANT: HOOK, Magnus A.O.
TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROWBIN-INDUCED COAGULATI
FILE REPERENCE: P07201UG01BAS
CURRENT APPLICATION NUMBER: US/10/142,935
CURRENT PILING DATE: 2002-05-13
PRIOR PEDLICATION NUMBER: US 60/290,072
PRIOR PEDLICATION NUMBER: US 60/290,072
PROFILE SEQ ID NOS: 11
SEQ ID NO 6
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Publication No. US2003004418A1
| Publication No. US2003004418A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: DAVIS, Stacey
| APPLICANT: DAVIS, Stacey
| APPLICANT: DAVIS, STACEY
| TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROWBIN-INDUCED COAGULATI
| TITLE OF INVENTION NUMBER: US/10/142,935
| CURRENT APPLICATION NUMBER: US 60/290,072
| PRIOR FILING DATE: 2001-05-13
| NUMBER OF SEQ ID NOS: 11
| SEQ ID NO 4
| SEQ ID NO 4
| LENGTH: 25
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TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
FILE REPERENCE: A35869 PCT USA A 071986.0248
CURRENT APPLICATION NUMBER: US/10/459,030B
CURRENT FILING DATE: 2003-06-11
PRIOR PLICATION NUMBER: PCT/AT01/00387
PRIOR PILING DATE: 2001-12-07
PRIOR PLICATION NUMBER: AT 2063/2000
PRIOR PILING DATE: 2001-12-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.0%; Score 41; DB 14; Length 25; 100.0%; Pred. No. 1.4;
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                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 294, Application US/10459030B
; Publication No. US20040192596A1
; GENERAL INFORMATION:
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Best Local Similarity 100.
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15 GHRPLDK 21
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US-10-142-935-4
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PRIOR APPLICATION NUMBER: US 09/695,360
PRIOR FILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 30
            FILING DATE: 2000-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
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31 GHRPLDK 37
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                                                                                                                                                                                                                                                                                             ; NAME/KEY: AMIDATION; LOCATION: 30
US-10-415-024-5
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US-09-919-039-33
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Publication No. US20040058984A1

GENERAL INFORMATION:

APPLICANT: Distide, Inc.

TITLE OF INVENTION: STABLILZATION OF RADIOPHARMACEUTICAL COMPOSITIONS

TITLE OF INVENTION: GIROMANS

FILE REPRENCE: 09744-015801

CURRENT APPLICATION NUMBER: US/10/415,024

CURRENT PILING DATE: 2003-04-24

PRIOR APPLICATION NUMBER: US 09/694,992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cyr, John B.

TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: 09744-017001
CURRENT PAPLICATION NUMBER: US/10/131,346
CURRENT APPLICATION NUMBER: US/09/695,360
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 30
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                                                                                                                                                                                                                                                                                         82.0%; Score 41; DB 14; Length 30; 100.0%; Pred. No. 1.7; Live 0; Mismatches 0; Indels
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PRIOR FILING DATE: 2001-10-24
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 30
                                                                                                                                                                   OTHER INFORMATION: Synthetic construct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 5, Application US/10131346; Publication No. US20030103899A1; GENERAL INFORMATION:
                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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GHRPLDK 10
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4 GHRPLDK 10
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LOCATION: 30
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US-10-415-024-5
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Sequence 1709, Application US/10276774

Publication No. US20040053245A1

GENERAL INFORMATION:

APPLICANT: Hyaeq, Inc.

TITLE OF INVENTION: No. US20040053245A1e1 Nucleic Acids and Polypeptides

FILE REPERENCE: 21272-030

CURRENT FILING DATE: 2002-11-18

PRIOR APPLICATION NUMBER: US/10/276,774

CURRENT FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: 09/496,914

PRIOR APPLICATION NUMBER: 09/496,914

PRIOR FILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 2700

SOFTWARE: CUSLOM

SEQ ID NO 1709
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Publication No. US20030108871A1
GENERAL INFORMATION:
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REPRENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
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CTHER INFORMATION: Xaa = any amino acid or nothing US-10-276-774-1709
                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                               OTHER INFORMATION: Synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 82.0%; Best Local Similarity 100.0%; Matches 7; Conservative 0
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 7; Conservative
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RESULT 14
US-10-42547
US-10-42547
Sequence 42547, Application US/10425114
Sequence 42547, Application No. US20040034888A1
Sequence 42547, Application No. US20040034888A1
GENERAL INFORMATION:
Sequence 42547, Application No. US2004003488A1
GENERAL INFORMATION:
APPLICANT: Exouption David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 42547
LENGTH: 248
TURE OF THE APPLICATION NUMBER OF SEQ ID NOS: 73128
TENGTH: 248
THE APPLICATION NUMBER OF SEQ ID NOS: 73128
TENGTH: 248
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ed Rosa, Thomas J.
APPLICANT: Ed Rosa, Thomas J.
APPLICANT: Ed Rosa, Thomas J.
APPLICANT: Edou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221)
FILE REPERENCE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 114771
LENGTH: 136
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                            Score 39; DB 11; Length 67;
Pred. No. 8.8;
1; Mismatches 1; Indels
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US-10-437-963-114771
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ORGANISM: Zea mays
ORGANISE:
OTHER INFORMATION: Clone ID: 700224123_FLI.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1)..(136)
OTHER INFORMATION: unsure at all Xaa locations
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; Sequence 114771, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
                                 Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
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Best Local Similarity 75...
6; Conservative
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57 GHVPLDRC 64
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Publication No. US20040009474A1

GENERAL INFORMATION:

APPLICANT: Leach, Martin D.

APPLICANT: Shimkets, Richard A.

TITLE OF INVENTION: NO. US20040009474A1e1 Human Polymucleotides and Polypeptides Encornance TITLE OF INVENTION: NO. US20040009474A1e1 Human Polymucleotides and Polypeptides Encornance TITLE OF INVENTION: NO. US20040009474A1e1 Human Polymucleotides and Polypeptides Encornance APPLICATION NUMBER: US/09/864,408A

CURRENT APPLICATION NUMBER: US/0266,690

PRIOR PRILING DATE: 2000-05-24

NUMBER OF SEQ ID NOS: 9068

SEQ ID NO 7552

LENGTH: 67
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; Sequence 6, Application US/1001724
; Publication No. US2003009958A1
GENERAL INFORMATION:
APPLICANT: MCZATLH, Jeanette
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
; CURRENT APPLICATION NUMBER: US/10/017,724
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/317,178
; PRIOR FILING DATE: 2001-05
; PRIOR FILING DATE: 2001-06
; RIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 11
; SOOTWARE: FREESEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 491
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100.0%; Pred. No. 26;
.ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 25;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                        NAME/KEY: misc feature; OTHER INFORMATION: Incyte ID No. US20030108871A1 3393861CD1
US-09-919-039-33
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL PROGRAM
SEQ ID NO 33
LENGTH: 488
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Best Local Similarity 100.
Matches 7; Conservative
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Matches 7; Conservative
                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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US-10-017-724-6
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CAGANISM: Homo sapiens
US-09-864-408A-7552
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US-09-864-408A-7552
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US-10-017-724-6
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Caro, Vinua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Buckharov, Plante Broback, Brad
APPLICANT: Broback, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221)8
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 12850
LENGTH: 493
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    Gaps
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APPLICANT: WESSLER, SUSAN R.
APPLICANT: JIANG, NING
APPLICANT: BAO, ZHIRONG
APPLICANT: ZHANG, XIAOYU
APPLICANT: ZHANG, XIAOYU
APPLICANT: SHANG, XIAOYU
APPLICANT: BDDY, SEAN R.
TITLE REFERENCE: 18465-0018
CURRENT APPLICATION NUMBER: US/10/346,198
CURRENT FILING DATE: 2003-01-16
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Pred. No. 94;
    Indels
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US-10-437-963-128550
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Pred. No. 1e+02;
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OTHER INFORMATION: unsure at all Xaa locations
  Mismatches
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                                                                                                                                                                                Sequence 128550, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/337,409
PRIOR FILING DATE: 2002-05-01
NUMBER OF SEQ ID NOS: 149
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 78
LENGTH: 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 78, Application US/10346198
Publication No. US20040043485A1
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Best Local Similarity 75.0
Matches 6; Conservative
  6; Conservative
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ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: unsure
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US-10-346-198-78
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Best Local Similarity
                                        1 GHRPLDKC
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  Matches
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thua
APPLICANT: Cao, Yongwei
APPLICANT: Roukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 187345
LENGTH: 352
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Publication No. US20040043485A1
GENERAL INFORMATION:
APPLICANT: WESSLER, SUGAN R.
APPLICANT: JIANG, NING
APPLICANT: ZHANG, XIRONG
APPLICANT: ZHANG, XIRONG
APPLICANT: EDDY, SEAN R.
TITLE OF INVENTION: TRANSPOSABLE ELEMENTS IN RICE AND METHODS OF USE
FILE REFRENCE: 18465-0018
CURRENT APPLICATION NUMBER: US/10/346,198
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                                      DB 15; Length 248; 48;
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Pred. No. 68;
                                                                              1; Indels
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US-10-437-963-187345
                                                                                1; Mismatches
                                      Score 38; Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/337,409
FRIOR FILING DATE: 2003-01-16
FRIOR FILING DATE: 2002-05-01
NUMBER OF SEQ ID NOS: 149
SOPTWARE: PatentIn Ver. 2.1
SEQ ID NO 29
LENGTH: 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 187345, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
                                      76.0%;
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Best Local Similarity 75.0°
                                    Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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CORGANISM: Oryza sativa
US-10-346-198-29
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29 GHRPLCRC 36
                                                                                                                      1 GHRPLDKC 8
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Best Local Similarity
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US-10-437-963-187345
US-10-425-114-42547
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US-10-346-198-29
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APPLICANT: Boukharov, Andrey A.;
APPLICANT: Boukharov, Andrey A.;
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
EMOTH: 257
TYPP: LEMOTH: 257
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Publication No. US20030233675A1

GENERAL INPORMATION:

APPLICANT: Stater, Steven C.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Glaman, Barry S.

APPLICANT: Glaman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Glaman, Barry S.

CURRENT APPLICATION NUMBER: US/10/369, 493

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360, 039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 6831

LENGTH: 482
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Pred. No. 1.4e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT4530_70938C.1.pep
US-10-437-963-172840
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Pred. No. 77;
0; Mismatches 2
                                                                                                                                                                        Sequence 172840, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Caenorhabditis elegans
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75.0%;
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85.7%;
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Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Oryza sativa
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                                                      1 GHRPLDKC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GHRPLDKC 8
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                                                                                                                                                           Sequence 187347, Application US/10437963

Sequence 187347, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Buckharov, Andrey A.
APPLICANT: By ing
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 187347

LENGTH: 626
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Jarbazuk, Brad

TITLE OF INVENTION: 11, Ping

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221) B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT PILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 187113

LENGTH: 136

TYPE: PING
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    2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: PAT_MRT4530_84059C.1.pep
US-10-437-963-187347
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US-10-437-963-187113
  0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 187113, Application US/10437963; Publication No. US20040123343A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
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Best Local Similarity 75.0
Matches 6; Conservative
  6; Conservative
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Matches 6; Conservative
                                                                              229 GHSPLQKC 236
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ORGANISM: Oryza sativa
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                                         1 GHRPLDKC 8
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US-10-437-963-187113
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Matches
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Sequence 5, Application US/10142935

Sequence 5, Application NS U10142935

Publication NO. US2003004418A1

GENERAL INFORMATION:
APPLICANT: DAVIS, Stacey
TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATI
FILE REFERENCE: PO7201US01/BAS
CURRENT FILIAG DATE: 2002-05-13
FRICH RAPLICATION NUMBER: US 60/290,072
FRICH RAPLICATION NUMBER: US 60/290,072
FRICH RAPLICATION NUMBER: US 60/290,072
FRICH REDEATE: 2001-05-13
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 5:
LENGTH: 20
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APPLICANT: LA ROSA, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT APPLICATION DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 132166
LENGTH: 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                            ; ORGANISM: Staphylococcus epidermidis
US-10-378-674-7
PRIOR APPLICATION NUMBER: 60/361,324
PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SRQ ID NO 7
LENGTH: 16
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ORGANISM: Oryza Bativa
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                       TYPE: PRT
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                                                                                           Sequence 9, Application US/10142935
Publication No. US20030044418A1
GENERAL INFORMATION:
APPLICANT: DAVIS, Stacey
APPLICANT: HOOK, Magnus A.O.
TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROWBIN-INDUCED COAGULATI
FILE REFERENCE: P07201US01/BAS
CURRENT APPLICATION NUMBER: US/10/142,935
CURRENT PILING DATE: 2002-05-13
PRIOR PILING DATE: 2001-05-13
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
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Subjection No. US20030044418A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DAVIS, Stacey
APPLICANT: DAVIS, Stacey
APPLICANT: HOOK, Magnus A.O.
TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATI
FILE REFERENCE: P07201US01/BAS
CURRENT APPLICATION NUMBER: US 60/290,072
PRIOR APPLICATION NUMBER: US 60/290,072
PRIOR FILING DATE: 2001-05-13
PRIOR FILING DATE: 2001-05-13
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
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Publication No. US2004000620911
GENERAL INFORMATION:
APPLICANT: PATTI, JOSEPH M.
TITLE OF INVENTION: MONOCLONAL AND POLYCLONAL ANTIBODIES RECOGNIZING COAGULASE-NEGATI
TITLE OF INVENTION: STAPHYLOCOCCAL PROTEINS
TITLE OF INVENTION: STAPHYLOCOCCAL PROTEINS
FILE REFERENCE: P07556US01/BAS
CURRENT APPLICATION NUMBER: US/10/378,674
CURRENT PILING DATE: 2003-03-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.0%; Score 36; DB 14; Length.10; 100.0%; Pred. No. 5.1; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.0%; Score 36; DB 14; Length 15; 100.0%; Pred. No. 7.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-142-935-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LENGTH: 15
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-142-935-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches, 6; Conservative
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GHRPLD 10
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Matches 6; Conserv
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US-10-142-935-8
                                                                         US-10-142-935-9
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US-10-378-674-7
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Shou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Branch Brad
APPLICANT: Brad
APPLICAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 735;
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US-10-437-963-182675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
72.0%; Score 36; DB 16;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 12627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 182675, Application US/10437963 ; Publication No. US20040123343A1 ; GENERAL INFORMATION:
                                                                                                                                                                                                                          Sequence 12627, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Streptomyces avermitilis
US-10-156-761-12627
                                                                                                                                                                                                                                                                                                                    APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               344 GHRPLD 349
                                                                             32 GHRPLD 37
                1 GHRPLD 6
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US-10-156-761-12627
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APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPERENCE: 38-21(5321)B

CURRENT APPLICATION NUMBER: 105/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 127165

LENGTH: 479

TYPE: ...
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 382, Application US/09864408A
Publication No. US20040009474A1
Publication No. US20040009474A1
GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Shimkets, Richard A.
TITLE OF INVERTION: No. US20040009474A1e1 Human Polynucleotides and Polypeptides Ence FILE REFERENCE: 21402-012.
CURRENT APPLICATION NUMBER: US/09/864,408A
CURRENT APPLICATION NUMBER: 06/206,690
PRIOR PEDICATION NUMBER: 60/206,690
PRIOR PEDICATION NUMBER: 60/206.05-24
NUMBER OF SEQ ID NOS: 9068
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 382
LENGTH: 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 72.0%; Score 36; DB 16; Length 479; Best Local Similarity 100.0%; Pred. No. 2.2e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                   72.0%; Score 36; DB 16; Length 90; 71.4%; Pred. No. 43; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
; OTHER INFORMATION: Clone ID: PAT_MRT4530_34161C.1.pep
US-10-437-963-132166
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US-10-437-963-127165
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.00
Then 6; Conservative
                                                                                                Query Match 72.0
Best Local Similarity 71.4
Matches 5; Conservative
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US-09-864-408A-382
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                              37 HRPIDAC 43
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Sequence 148809, Application US/10437963
; Sequence 148809, Application US 10437963
; Publication No. US20040123343A1
; Publication No. US20040123343A1
; GENERAL INFORMATION:
    APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
; APPLICANT: APPLICANTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERRACE: 38-21(53221)B
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 148809
; LENGTH: 111

**WUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 148099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Shou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wei
APPLICANT: Bunkharov, Andrey A.
APPLICANT: Bunkharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 129796
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70.0%; Score 35; DB 16; Length 111;
Best Local Similarity 71.4%; Pred. No. 82;
Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35; DB 16; Length 131;
Pred. No. 96;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_49202C.1.pep
US-10-437-963-148809
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US-10-437-963-129796
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Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Oryza sativa
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     41 HRPLDK 46
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                                                                                                                                                                                                                         APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, wei
APPLICANT: Wu, wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Plant and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 10/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 114710
LENGTH: 800
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Bublication No. US20040031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
Cao Yongwei
APPLICANT:
Cao Yongwei
TITLE OF INVENTION:
Plants and Uses Thereof for Plant Improvement
FILE OF INVENTION:
FILE SEFERENCE:
38-21(53.23)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE:
2003-04-28
NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 175814

LENGTH: 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.0%; Score 36; DB 16; Length 800; 71.4%; Pred. No. 3.6e+02; ive 2; Mismatches 0; Indels
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US-10-424-599-175814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: PAT_MRT4530_18374C.1.pep
US-10-437-963-114710
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OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                        ; Sequence 114710, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 72.0
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||||::|
243 HRPLEEC 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 HRPLDKC 8
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94 GHRPLD 99
                                                                                                       RESULT 32
US-10-437-963-114710
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70.0%; Score 35; DB 14; Length 305; 100.0%; Pred. No. 2.2e+02;
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         Sequence 450, Application US/10017161
| Publication No. US20030143668A1
| GENERAL INFORMATION:
| APPLICANT: SUWA, MAKIKO
| APPLICANT: ARIYAMA, YUTAKA
| APPLICANT: ARIYAMA, YUTAKA
| APPLICANT: ABURATANI, HIROYUKI
| TILLE OF INVENTION: NOWELG PROTEIN-COUPLED RECEPTORS
| FILE REFERENCE: 084335/0152
| CURRENT FILING DATE: 2002-12-18
| PRIOR FILING DATE: 2001-06-18
| WINGBR OF SEQ ID NOS: 2430
| SOFTWARE: Patentin Ver: 2.1
| SEQ ID NO 450
| TENDER 1305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 466, Application US/10017161
Publication No. US20030143668A1
GENERAL INFORMATION:
APPLICANT: SUMA, MAXINO
APPLICANT: AAXIYAMA, YUTAKA
APPLICANT: AAXIYAMA, YUTAKA
APPLICANT: ABUMATINI, HUROVUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT FILING DATE: 2002-12-18
PRIOR FILING DATE: 2001-66-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.0%; Score 35; DB 14; 100.0%; Pred. No. 2.2e+02; ive 0; Mismatches 0;
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Publication No. US20030198955A1
GENERAL INFORMATION:
APPLICANT: Li, Li
APPLICANT: Padigaru, Muralidhara
APPLICANT: Relianger, Robert
APPLICANT: Relianger, Robert
APPLICANT: Relianger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 70.0
Best Local Similarity 100.
Matches 6; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 468
LENGTH: 305
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Best Local Similarity 100.
Matches 6; Conservative
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CRGANISM: Homo sapiens
US-10-017-161-468
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US-10-017-161-450
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US-10-017-161-450
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Sequence 68291, Application US/10425114

GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yibua
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Ynongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE OF INVENTION NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28

SEQ ID NOS: 73128

EENGTH: 275
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75.0%; Pred. No. 2e+02;
.ive 0; Mismatches 2; Indels
                                                                      Sequence 1356, Application US/10017161
Sequence 1356, Application US/10017161
Sequence 1356, Application US/10017161
GENERAL INFORMATION:
APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: ARIXANA, YUTAKA
APPLICANT: ARIXANA, YUTAKA
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REPERENCE: 084335/0152
CURRENT FILING DATE: 2002-12-18
PRIOR PILING DATE: 2001-06-18
PRIOR PILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-06-18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1358
LENGTH: 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Clone ID: UC-ZMFLMO17266H05_FLI.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MOD_RES
LOCATION: (8) ... (41)
COTHER INFORMATION: Variable amino acid
US-10-017-161-1358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 GHRPLVAC 133
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155 HRPLDK 160
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 37
US-10-425-114-68291
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RESULT 38

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Gaps

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THE SECTION OF STATES AND STATES 
Casman, Stacie
Edinger, Shlomit
Gerlach, Valerie
Sciore, Paul
Smithson, Glennda
Peyman, John
MacDougall, John
Stone, David
```

Search completed: June 1, 2005, 11:57:10 Job time : 100.733 secs

|||||| 220 HRPLDK 225

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

June 1, 2005, 11:41:15; Search time 25.6 Seconds (without alignments) 30.068 Million cell updates/sec Run on:

US-09-424-940A-2 50

1 GHRPLDKC 8 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	fibrinogen beta ch	fibrinogen beta ch	protein F18014.27	hypothetical prote	hypothetical prote	probable cytochrom	hypothetical prote	probable transcrip	hypothetical prote	fibrinogen beta ch	multi resistance p	fibrinogen beta ch	hypothetical prote	probable UDP-gluco	suppressor protein	alpha-amylase/tryp	trans-activating t	trans-activating t	probable integrase	probable integrase	hypothetical prote	zinc finger protei	phospholipase A2 (hypothetical prote	hypothetical prote	pol protein - yeas	MutT/nudix family		polymerase epsilon
SUMMARIES	ΩI	A05297	FGHUB	A86328	D82773	T15829	B84514	873790	C95399	AE2632	FGBOB	T47840	A38463	T27807	D96499	T18307	WIILAI	TNLJGG	S12157	F90825	A85684	T29789	T40817	JC7284	A84608	T29134	T03277	A75550	H95278	AD2936
	8	~	-	~	7	7	~	7	7	~	Н	N	~	~	7	~	Н	Н	0	7	0	N	~	7	0	~	N	N	~	7
	Query Match Length	31	491	725	82	482	518	591	201	240	468	1490	463	295	615	101	122	130	130	409	416	421	673	782	795	911	1576	225	325	326
de	Query	82.0	82.0	78.0	74.0	74.0	74.0	74.0	72.0	72.0	72.0	72.0	70.0	70.0	70.0	70.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	0.99	0.99	0.99
	Score	41	41	39	37	37	37	37	36	36	36	36	35	. 35	35		34	34	34		34	34	34	34	34	34	34	33	33	33
	Result No.	-	7	E)	4	5	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

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hypothetical prote zinc transporter z methionine gamma-l	methionine gamma-1 probable phok prot ankyrin-like prote chitinase (EC 3.2.	trans-activating t hypothetical prote conserved hypothet hypothetical prote hypothetical prote	hypothetical prote glycosyltransferas hypothetical prote hypothetical prote
C98346 T52184 AB3025	G98259 A70706 D82654 T14075	S46349 T17674 E82256 B71305 S40749	H81291 F97257 T23182 T20233
0 0 0	00000	00000	0000
326 353 427	427 485 1058 1635	116 189 296 309	372 374 383 423
66.0 66.0	0.000 0.000 0.0000 0.0000	64.0 64.0 64.0 64.0	64.0 64.0 64.0 64.0
		N	2222 2222
3310	. 4 . 0 . 0 . 1	3 6 6 4 4 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	4 4 4 4 2 6 4 2

ALIGNMENTS

RESULT 1

fibringen beta chain - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Accession: B94308; A03123; A7512; A05297; B37512; D03118
R;Birken, S.; Wilner, G.D.; Canfield, R.E.
Thromb. Res 7, 599-610, 1975
A;Ttle: Studies of the structure of canine fibrinogen.
A;Reference number: A94308; MUID:76081726; PMID:1198547

A; Accession: B94308

A; Molecule type: protein A; Residues: 1-31 cBIR» A; Cross-references: UNIPROT: P02677 R; Blombaeck, B.; Blombaeck, M.; Groendahl, N.J. Acta Chem. Scand. 19, 1789-1791, 1965 A;Tttle: Studies on fibrinopeptides from mammals.

A; Reference number: A03118 A; Accession: A03123

A,Molecule type: protein A,Residues: 1-19 <BLO> R,Krajewski, T.; Blomback, B. Acta Chem. Scand. 22, 1339-1346, 1968 A,Reference number: A37512; MUID:69066367; PMID:5727635

A;Accession: A37512 A;Molecule type: protein A;Residues: 1-19 <KRA>

Gaps ö 82.0%; Score 41; DB 2; Length 31; 100.0%; Pred. No. 0.22; 0; Indels Local Similarity 100.0%; Pred. No. 0.2 nes 7; Conservative 0; Mismatches Query Match Best Loc Matches

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ò 셤 RESULT 2

fibrinogen beta chain precursor [validated] - human

NyAlternate names: coagulation factor I NyContains fibrinopeptide B CyContains fibrinopeptide B CyContains fibrinopeptide B CyContains fabrinopeptide B CyContains Barbes, Raydes, Baydes, Baydes, Baydes, A94433; A90437; A94309; G54223; A03121; B37 RyChung, D.W.; Harris, J.E.; Davie, E.W. Adv. Exp. Med. Biol. 281, 39-48, 1990

2

```
R;Kirschbaum, N.E.; Budzynski, A.Z.
J. Biol. Chem. 265, 13669-13676, 1990
A;Title: A unique proteolytic fragment of human fibrinogen containing the Aalpha COOH-te:
A;Reference number: A37117; MUID:90337977; PMID:2143188
A;Contents: annotation; hementin cleavage site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Note: hementin, a protease from Haementeria ghilianii, the giant South American leech, C; Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves istation sites responsible for the formation of the soft clot.
C; Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabilized) and between alpha chains (weaker) of different monomers.
C; Comment: All fibrinogen chains are synthesized in the liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GDB:119130; OMIM:134830
A;Map position: 4q28-4q28
A;Introns: 38/3; 102/3; 164/1; 240/1; 278/1; 415/2
A;Introns: 38/3; 102/3; 164/1; 240/1; 278/1; 415/2
C;Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:FGF) ins are contained in the core. Two three-chain coiled coils emerge from this core and core from the distal domain nodes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lymuction: fibrinogen cleaved by thrombin yields monomers that are polymerized into farbathway: blood coagulation

CySuperfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfic CySuperfamily: fibrinogen beta chain; fibrinogen beta special coil; glycoprotein; liver; plasma; pyroglutamic acus F;1-30/Domain: (or 4-30 or 15-30) signal sequence #status predicted «SIG»

F;31-491/Product: fibrinogen beta chain #status experimental «MAT»

F;31-491/Product: fibrinopeptide B #status experimental «APT»

F;45-491/Product: fibrinopeptide B #status experimental «PGB»

F;45-491/Product: fibrinopeptide B #status experimental «PGB»

F;45-491/Product: fibrinopeptide B #status experimental «Fibrinopen disulfide ring homology «FDR»

F;328-487/Domain: fibrinogen disulfide mid (Gln) (in mature form) #status experimental

F;31/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental

F;34-45/Cleavage site: Arg-Gly (thrombin) #status experimental

F;106/Disulfide bonds: interchain (to alpha-65) #status experimental

F;106/Disulfide bonds: interchain (to gamma-45) #status experimental

F;227/Disulfide bonds: interchain (to gamma-45) #status experimental

F;237/Bianfide bonds: interchain (to gamma-45) #status experimental

F;227/Disulfide bonds: interchain (to gamma-161) #status experimental

F;237/Bianfide bonds: interchain (to gamma-161) #status experimental

F;237/Bianfide bonds: interchain (to gamma-161) #status experimental
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CiSpecies: Assolut #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
CiAccession: As6328
RiTheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chi, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Anture 408, 816-820, 2000
A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Marti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
       Annu. Rev. Biochem. 53, 195-229, 1984

A;Title: Fibrinogen and fibrin.

A;Reference number: A90041; MUID:84305751; PMID:6383194

A;Contents: annotation; review, EM structure, polymerization, ligands R;Chung, D.W.; Rixon, M.W.; Que, B.G.; Davie, E.W.
Ann. N. Y. Acad. Sci. 408, 449-456, 1983

A;Title: Cloning of fibrinogen genes and their cDNA.

A;Reference number: A90038; MUID:83254384; PMID:6575700
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Best Local Similarity 100...
7, Conservative
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A,Reference number: A90469, MUID:83283433; PMID:6688356
                                                                                                                                                                                                                                                                                                                                                    A;Accession: A90469
A;Accession: A90469
A;Molecule type: DNA
A;Residues: 1-38 < CH1>
A;Accession: B90469
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 9-191, 'A',193-491 < CH2>
A;Cross-references: GB:J00129; NID:g182429; PIDN:AAA52429.1; PID:g182430
A;Cross-references: GB:J00129; NID:g182429; PIDN:AAA52429.1; PID:g182430
A;TitLe: Characterization of the 5'-flanking region for the human fibrinogen beta gene.
A,Title: Nucleotide sequences of the three genes coding for human fibrinogen. A;Reference number: A43568; MUD:91344740; PMID:2102623
A;Accession: B43568
A;Molecule type: DNA
A;Residues: 9-191,'P',193-491 <CHU>A;Cross-references: UNIPROT:P02675
B;Crhung, D.W.; Que, B.G.; Rixon, M.W.; Mace Jr., M.; Davie, E.W.
Biochemistry 22, 3244-3250, 1983
A;Title: Characterization of complementary deoxyribonucleic acid and genomic of
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: Loun
A;Molecule type: Loun
A;Residues: 1-482 - AEND-
A;Cross-references: UNIPROT: 009937; EMBL: U28734; NID: 9861255; PID: 91945480; PIDN: AAB5260
A;Experimental source: strain Bristol N2; clone C53C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q9S149; GB:AE002093; NID:g4587680; PIDN:AAD25850.1; GSPDB:GN:
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A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae A;Reference number: S73327; MUD:97105885; PMID:8948633
A;Accession: S73790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
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A,Introns: 19/2; 49/3; 128/3; 189/2; 203/3; 254/3; 273/1; 311/2; 372/2; 449/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable cytochrome P450 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
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Pred. No. 21;
2; Mismatches
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Best Local Similarity 62.5
Matches 5, Conservative
                       A; Reference number: 218413
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tes 6; Conserv
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A;Molecule type: DNA
A;Residues: 1-518 <STO>
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A; Residues: 1-591 <HIM>
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A, Experimental source: strain 9a5c
A, Experimental source: strain 9a5c
A, Eximpson, A.JG.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Bocena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to Genbank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.W.F.; Marino, C.L.; Marques, M.V.; Martins, E. A; Authors: Matrins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Silva, M.C.; Pelmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A; Tsuharor: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., M.A.; da Silvain, A.B.; Z.
B. Pefacorora manda, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z.
                                                                                                                                                                                                                                         A,Cross-references: UNIPROT:Q9LM43; GB:AE005172; NID:g8778424; PIDN:AAF79432.1; GSPDB:GM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Species: Xylella fastidiosa
C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C; Accession: D82773
R; Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A; Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A; Reference number: A82515; MUID: 20365717; PMID: 10910347
A; Note: for a complete list of authors see reference number A59328 below
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hypothetical protein C53C9.3 - Caenorhabdills closed to the C55C9.3 - Caenorhabdills clegans
C;Species: Caenorhabdilis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15829
R;Bentley, D.
Submitted to the EMBL Data Library, June 1995
A;Description: The sequence of C. elegans cosmid C53C9.
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ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A86328
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-725 <STO>
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Pred. No. 12;
1; Mismatches 1; Indels
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Pred. No. 3.5;
0; Mismatches 2
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75.0%;
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Best Local Similarity 75.0
Matches 6; Conservative
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555 GHKPDDKC 562
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Best Local Similarity
Matches 6; Conserv
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C;Genetics:
A;Gene: XF0702
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A;Molecule type: DNA
A;Residues: 1-82 <SIM>
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A;Accession: B03117
A;Molecule type: protein
A;Rolecule type: protein
A;Rolecule type: 5-21 & S. Rubira, M.R.; Hageman, T.C.; Hurrell, J.G.R.; Leach, S
A;Artinelli, R.A.; Inglis, A.S.; 1979
A;Title: Amino acid sequences of portions of the alpha and beta chains of bovine fibrinoc
A;Reference number: A37507; MUID:79164394; PMID:434821
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A; Molecule type: protein
A; Residues: 373-374 cMED.
C; Comment: Thrombin cleaves the bond between Arg-21 and Gly-22 to release fibrinopeptide
C; Comment: Thrombin cleaves the bond between Equal to three nonidentical chains (alphic; C; Comment: Pibrinogen betwo chain; fibrinogen betwickness betwo chain; fibrinogen betwickness by C; Keywords: blood coagulation; glycoprotein; plasma; pyroglutamic acid; sulfoprotein
F; 76-205/pomain: fibrinogen disulfide ring homology <PDR>
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A;Moslecule type: protein
R;Rssidues: 22-53 «MAR»
R;Chung, D.W.; Rixon, M.W.; MacGillivray, R.T.A.; Davie, E.W.
R;Chung, D.W.; Rixon, M.W.; M466-1470, 1981
Proc. Natl. Acad. Sci. U.S.A. 78, 1466-1470, 1981
Proc. Natl. Acad. Sci. U.S.A. 78, 1466-1470, 1981
A;Title: Characterization of a cDNA clone coding for the beta chain of bovine fibrinogen
A;Reference number: A37513; MUID:81199473; PMID:6262803
A;Accession: A37513
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A; Residues: 44-468 < CHU>
R; Medved, L.V.; Platonova, T.N.; Litvinovich, S.V.; Lukinova, N.I.
FEBS Lett. 232, 56-60, 1988
A; Title: The cleavage of beta-chain in bovine fibrinogen D(H) fragment (95 kDa) leads to
A; Réference number: $02443; MUID:88211875; PMID:2966748
                                                                                                                                                                                                                                                                                                                                                                                                                                     Nicontains: fibrinopeptide B
C;Species: Bos prinidenius taurus (cattle)
C;Species: 29-Jul-1981 #sequence revision 29-Jul-1981 #text_change 13-Sep-1996
C;Accession: A03122; B03117; B37507; A37513; S02443
R;Blomback, B.; Doolittle, R.F.
Acta Chem. Scand. 17, 1816-1819, 1963
A;Tille: The sequence of amino acids at the N-terminal end of bovine fibrinopeptide A;Reference number: A03122
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F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;6/Binding site: sulfate (Tyr) (covalent) #status experimental
F;21-22/Cleavage site: Arg-Gly (thrombin) #status experimental
F;311/Binding site: carbohydrate (Ann) (covalent) #status predicted
F;312-373/Cleavage site: Arg-Thr (plasmin) #status experimental
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                                   Length 240;
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A,Residues: 1-4 <BLO>
R;Sjoquist, J.; Blomback, B.; Wallen, P.
Ark. Kemi 16, 422-436, 1960
A;Title: Amino acid sequence of bovine fibrinopeptides.
A;Reference number: A03117
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Pred. No. 30;
0; Mismatches
                                   Score 36; DB
Pred. No. 16;
0; Mismatches
                               n 72.0%;
Similarity 85.7%;
6; Conservative
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85.7%;
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                                      Query Match
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Best Local Similarity
Matches 6; Conserv
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C95399
probable transcription regulator [imported] - Sinorhizobium meliloti (strain 1021) magap
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: C95399
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
B; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot
A;Reference number: A95262; MUID:21396509; PMID:11481432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule Lype: DNA
A; Residues: 1-201 «KUR»
A; Residues: 1-201 «KUR»
A; Cross-references: UNIPROT: Q92XY9; GB: AE006469; PIDN: AAK65757.1; PID: g14524255; GSPDB: G
A; Experimental source: strain 1021, megaplasmid pSymA
B; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A; Atchors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, B.; Komp, C.; Lelaure,
hebault, P.; vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A; Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A; Reference number: A96039; MUID: 21368234; PMID: 11474104
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AB2632
hypothetical protein Atu0456 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AB2632
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
S;Carpe, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q8U144; GB:AE008688; PIDN:AAL41475.1; PID:g17738801; GSPDB:A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu0456
A;Map position: circular chromosome
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A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
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C, Superfamily: Mycoplasma pneumoniae hypothetical protein A19_ORF591
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                                                                      Score 37; DB 2; Length 591;
Pred. No. 24;
                                                                                                                                        Indels
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                                                                  74.08;
75.08;
                                   Ouery Match
Best Local Similarity 75.0
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-240 < KUR>
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A;Genome: plasmid
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Query Match

Matches

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0; Mismatches
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Pred. No.
A; Experimental source: clone ZK265 C; Genetics:
A; Gene: CESP: ZK265.1
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Best Local Similarity 75.0°
                                                                                                                                                                                                           Query Match
Best Local Similarity 62.5
Matches 5; Conservative
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404 GYRPIDYC 411
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A;Molecule type: DNA
A;Residues: 1-615 <STO>
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A;Gene: T10P12.7
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A;Reference number: 220422
A;Accession: T27807
A;Accession: T27807
A;Accession: T27807
A;Molecule type: DNA
A;Residues: 1-562 <WILL>
A;Coss-references: UNIPROT:Q94400; EMBL:Z81143; PIDN:CAB03514.1; GSPDB:GN00019; CESP:ZM
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                                                                                                     N'Alternate names: protein T209.140
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47840
C;Accession: Farmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.; submitted to the Protein Sequence Database, Pebruary 2000
A;Reference number: Z24475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 3
A;Introns: 9/1; 795/3; 824/3; 1036/3; 1075/3; 1174/1; 1245/3; 1347/3; 1369/1; 1449/1
A;Note: T209.140
C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27807
R;Dobson, R.
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100.0%; Pred. No. 90;
iive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                           A; Accession: T47840
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-1490 < NYA>
A; Croser references: UNIPROT: Q9MIC7; EMBL: AL138658
A; Experimental source: cultivar Columbia; BAC clone T209
C; Genetics:
                                                                       resistance protein homolog - Arabidopsis thaliana
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les 6; Conservative
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Matches 6; Conservative
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Chin, C.W.; Chung, M.K.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Mature 408, 816-820, 2000
A,Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, E.; Kim, C.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Schun, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A,Fitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A,Reference number: A86141; MuID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q9XIG1, GB:AE005173; NID:g5080759; PIDN:AAD39269.1; GSPDB:GN(
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Yeast 14, 77-87, 1998
A;Title: Kluyveromyces lactis SEP1 and its Saccharomyces cerevisiae homologue bypass the A;Refere number: Z13599; MUID:98144791; PMID:9483797
A;Recession: T18307
A;Status; preliminary; translated from GB/EMBL/DDBJ
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A;Cross-references: UNIPROT:P87164; EMBL:U92898; NID:g2104692; PID:g2104693; PIDN:AAC3935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable UDP-glucose, sterol glucosyltransferase [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (5.5pecies: Arabidopsis thaliana (mouse-ear cress) (5.5pecies: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 (5.Accession: D96499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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C;Species: Kluyveromyces marxianus var. lactis, Candida sphaerica
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Aug-2004
                                                                                                                                                                                                            Gaps
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A;Map position: 1
A;Introns: 19/2; 46/3; 93/2; 219/2; 274/3; 319/2; 362/3; 431/3; 482/1
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                                                                                                            Score 35; DB 2; Length 562;
Pred. No. 55;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 615;
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C;Superfamily: GAL4 zinc binuclear cluster homology
F;81-121/Domain: GAL4 zinc binuclear cluster homology <GL4>
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us-09-424-940a-2.rpr

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A;Title: Nucleotide sequence of HIV-2(D194), an isolate from a Gambian case of 'Neuro-All. A;Reference number: S12152; MUID:91045094; PMID:2235509
A;Accession: S12157
A;Accession: S12157
A;Accession: D1257
A;Molecule type: DNA
A;Molecule type: DNA
A;Rose-references: UNIPROT:P17759; EMBL:X52223; NID:960155; PIDN:CAA36469.1; PID:9763106; A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable integrase [imported] - Escherichia coli (strain 0157:H7, substrain RIMD 0509952)]
C;Species: Bscherichia coli
C;Species: Bscherichia coli
C;Accession: F90825
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; gasawara, N.; Yashunga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomia A;Accession: F90825
A;Accession: F90825
A;Status: preliminary
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A;Residues 1.409 cHAX-
A;Cross-references: UNIRROT:08X775; GB:BA000007; PIDN:BAB34997.1; PID:g13361038; GSPDB:GN-
A;Experimental source: strain O157:H7, substrain RIMD 0509952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CjAccession: A85684
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, iller, L.; Grotbeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
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A,Introns: 99/2
A,Introns: 99/2
C,Superfamily: AIDS trans-activating transcription regulator
C,Keywords: transcription regulation
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Pred. No. 64;
0; Mismatches
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A,Gene: ECs1574
C,Superfamily: phage phi-80 integrase
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C;Superfamily: phage phi-80 integrase
Nucleic Acids Res. 18, 6142, 1990
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44 HRPLEAC 50
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Best Local Similarity
Matches 6; Conserv
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Matches
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                                                                                                                                                                                                                                                                                                       alpha-amylase/trypsin inhibitor - finger millet
C;Species: Bleusine coracan (finger millet)
C;Date: 18-Apr-1984 #sequence_revision 18-Apr-1984 #text_change 09-Jul-2004
C;Accession: A01326
R;Campos, F.A.P.; Richardson, M.
FPBS Lett. 152, 300-304, 1983
A;Title: The complete amino acid sequence of the bifunctional alpha-amylase/trypsin inhi
A;Reference number: A01326
A;Accession: A01326
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Ribasegawa, A.; Tsujimoto, H.; Maki, N.; Ishikawa, K.; Miura, T.; Fukasawa, M.; Miki, K. Marisegawa, A.; Tsujimoto, H.; Maki, N.; Ishikawa, K.; Miura, T.; Fukasawa, M.; Miki, K. Misses and Hum. Retroviruses 5, 593-604, 1989
A;Title: Sequence of a distinct HIV-2 isolate from Ghana showing significant divergence A;Reference number: JS0327; MUD: 90122350; PMID: 2611042
A;Accession: JS0332
A;Accession: JS0332
A;Accession: JS0332
A;Residues: 1-130 <HAS>
A;Residues: 1-130 <HAS>
A;Cross-references: UNIPROT: P18044; GB: M30895; GB: D00477; NID: G325709; PIDN: AAA43929.1;
C;Genetics:
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C,Species: human immunodeficiency virus type 2, HIV-2
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S12157
R;Kuehnel, H.; Kreutz, R.; Ruebsamen-Waigmann, H.
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A; Residues: 1-122 < CAM>
A; Residues: 1-122 < CAM>
A; Cross-references: UNIPROT: P01087
A; Cross-references: UNIPROT: P01087
C; Superfamily: wheat alpha-amylase inhibitor
C; Reywords: alpha-amylase inhibitor
C; Keywords: alpha-amylase inhibitor
F; 34/Inhibitory site: Arg (trypsin) #status predicted
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Pred. No. 21;
1; Mismatches 1; Indels
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C;Superfamily: AIDS trans-activating transcription regulator
C;Keywords: AIDS; transcription regulation
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Local Similarity 71.4%;
Les 5; Conservative 1
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GHRPVTSC 86
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HRPLEAC 50
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Rilin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
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A;Residues: 1-795 <STO>
A;Cross-references: UNIPROT:Q9SIZ7; GB:AE002093; NID:g4417294; PIDN:AAD20419.1; GSPDB:GN
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A;Experimental source: strain Bristol N2; clone C09D4
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A;Introns: 27/1; 55/2; 89/1; 117/2; 187/3; 232/1; 284/1; 356/2; 380/3; 430/3; 492/1; 527,
                            Firanaka, H.; Takeya, R.; Sumimoto, H.
Biochem. Biophys. Res. Commun. 272, 320-326, 2000
A; Title: A novel intracellular membrane-bound calcium-independent phospholipase A2.
A; Reference number: JC7284
A; Rocession: JC7284
A; Rosidues: 1-782 *TANA
A; Residues: 1-782 *TANA
A; Residues: 1-782 *TANA
A; Residues: J-782 *TANA
A; Residues: JC784 *TAN
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C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: A84608
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels
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submitted to the RMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid C09D4
A;Reference number: Z20576
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A;Molecule type: DNA
A;Residues: 1-911 <MUX>
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41 GHRPLER 47
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C; Accession: JC7284
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A;Map position: 2
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R;Beck, A.; Reinhardt, R.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
Bubmitted to the EMBL Data Library, October 1998
A;Accession: T40817
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residuse: 1-673 < BEC.
A;Residuse: 1-673 < BEC.
A;Residuse: 1-673 < CBC.
A;Experimental source: strain 972h-; clone pl p887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F44A2.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Dacte: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29789
R;Du, Z.; Le, T.
Submitted to the RMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid F44A2.
A;Reference number: Z20686
A;Reference number: Z20686
A;Accession: T29789
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JC7284
phospholipase A2 (EC 3.1.1.4) 2, calcium-independent - human
N;Alternate names: membrane-associated calcium-independent phospholipase A2
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
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C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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                                Score 34; DB 2; Length 416;
Pred. No. 65;
0; Mismatches 2; Indels
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A;Gene: CESP:F44A2.2
A;Introns: 144/3; 224/2; 278/1; 328/1
                            Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
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160 GHHPMDK 166
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C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: H95270
E;Accession: H95270
E;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse is Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C., Proce, Natl. Acad. Sci. US.A., 98, 988-9888, 2001
E;Alt.le: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloting A;Reference number: A95262; MUID:21396509; PMID:11481432
                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-325 -KUR>
A; Residues: 1-325 -KUR>
A; Cross-references: UNIPROT: 093009; GB: AE006469; PIDN: AAK64794.1; PID: g14523204; GSPDB: GNA: A; Experimental source: strain 1021, megaplasmid pSymA. Abola, P.; Ampe, F.; Barloy-Hubler, A; Abola, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 293, 668-672, 2001

A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, Abauthors: Kahn, D.; Kahn, M.L.; Worder, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.Claritle: The composite genome of the legume symbiont Sinorhizobium meliloti.

A; Reference number: A96039; MUID:21368234; PMID:11474104

A; Contents: annotation
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C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AD2936
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A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, F.
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hypothetical protein AGR L_3437 [imported] - Agrobacterium tumefaciens (strain C58, Cerec
C;Species: Agrobacterium tumefaciens
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A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; WUID:21608550; PMID:11743193
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Matches 5; Conservative
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Matches 5; Conservative
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MutT/mudix family protein - Deinococcus radiodurans (strain R1)

C,Species: Deinococcus radiodurans

C,Species: Deinococcus radiodurans

C,Baccies: Deinococcus radiodurans

C,Baccies: Deinococcus radiodurans

C,Baccies: Deinococcus radiodurans

C,Baccies: Deinococcus radiodurans

C,Accession: A7550

R,White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

M, Shith, H.O.; Vomathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Vonter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A,Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A,Reference number: A75250; MUID:20036896; PMID:10567266

A,Recession: A75550

A,Statuus: preliminary
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       C; Superfamily: Caenorhabditis elegans hypothetical protein C09D4.4
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Pred. No. 1.4e+02;
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Pred. No. 2.4e+02;
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                                                                                       Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 71.4%;
Matches 5; Conservative
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C,Superfamily: NUDIX hydrolase
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Matches 6; Conservative
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1506 HRPIDIC 1512
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A; Residues: 1-225 <WHI>
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H95278
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A;Cross-references: UNIPROT:Q8U9C2; GB:AE008689; PIDN:AAL44616.1; PID:g17742238; GSPDB:G3 A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;App position: linear chromosome
C;Superfamily: O-succinylhomoserine (thiol)-lyase
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A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume A;Reference number: A97359; MUID:21608551; PMID:11743194
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A;Cross-references: UNIPROT:P71815; GB:Z80226; GB:AL123456; NID:g3261638; PIDN:CAB02401.1
A;Experimental source: strain H37Rv
C;Genetics:
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Alvathors: Sqares, R.; Sullston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
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C,Species: Mycobacterium tuberculosis
C,Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
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Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels
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C;Superfamily: O-succinylhomoserine (thiol)-lyase
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-427 <KUR>
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                                           C;Accession: C98346
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, P.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 23, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
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C;Genetics:
A;Gene: AGR L. 3437
A;Map postition: linear chromosome
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A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   methionine gamma-lyase mdeA [imported] - Agrobacterium tumefaciens (strain C58, Dupont) C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #text change 09-Jul-2004
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A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
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          C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
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Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
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Pred. No. 81;
1; Mismatches 2; Indels
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88;
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A;Molecule type: mRNA
A;Residues: 1-353 <GRO>
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Best Local Similarity 62.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 GHRAVDDC 221
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320 GYKPLEEC 327
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                                                                                                                                                                                                                                                                                                                                                                  A;Accession: C98346
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-326 <KUR>
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A;Molecule type: DNA
A;Residues: 1-427 <KUR>
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A'Variety: isolate SAB-1
C;Date: 25-Dec-1994 #sequence_revision 14-Feb-1997 #text_change 20-Sep-1999
C;Accession: S46349
R;Jin, M.J.; Hui, H.; Robertson, D.L.; Mueller, M.C.; Barre-Sinoussi, F.; Hirsch, V.M.; J.
EMBO J. 13, 2935-2947, 1994
A;Title: Mosaic genome structure of simian immunodeficiency virus from West African greer!
A;Reference number: S46335; MUID:94298785; PMID:8026477
                                                                                                                                                                                                                                                                                           trans-activating transcription regulator - simian immunodeficiency virus SIVagm (isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conserved hypothetical protein VC0975 [imported] - Vibrio cholerae (strain N16961 serogro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:U04005; NID:9466229; PIDN:AAA21507.1; PID:9466233
A;Experimental source: isolate SAB-1; sabaeus monkey
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1993
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A;Accession: T17674
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-116 <GRA>
A;CRAS=references: UNIPROT:Q84504; EMBL:U42580; NID:g4028896; PIDN:AAC96552.1
A;Experimental source: specific host Chlorella strain NC64A
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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C;Species: Chlorella virus PBCV-1
C;Species: Chore-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T1767, Van Etten, J.L.
R;Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
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C,Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C,Accession: E82256
                Gaps
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A;Status: nucleic acid sequence not shown; translation not shown
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A;Note: a184L
C;Superfamily: Chlorella virus PBCV-1 hypothetical protein A184L
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Pred. No. 47;
2; Mismatches 1; Indels
            Indels
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C,Superfamily: AIDS trans-activating transcription regulator
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Pred. No. 30;
0; Mismatches
            Mismatches
                                                                                                                                                                                                                                                                                                                           N;Alternate names: tat protein
C;Species: simian immunodeficiency virus SIVagm
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71.4%;
            5; Conservative
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 4; Conserv
                                                                                                          ||:|||
54 RPVDKC 59
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A; Residues: 1-73 <JIN>
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                                                                          3 RPLDKC
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A;Gene: tat
            Matches
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                                                                                                                                                                                                                                                                                                    CiSpecies: Xylella fastidiosa
CiDate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
CiAccession: D82654
R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 200
A; Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A; Reference number: A82515; MuID:20365717; PMID:10910347
A; Rocession: D82654
A; Status preliminary
A; Molecule type: DNA
A; Residues: 1-1058 <SIM>A; Residues: 1-1058 <SIM>A; Residues: 1-1058 CSIM
A; Remper, B.L.; Kitajima, J.P.; Krieger, J.S.; Ferraira, A.J.S.
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.Y.; Martins, E.R.F.; Matsukuma, A.Y.; Mence, C.F.M.; Mirack, C.P.; Pilmartins, E.M.F.; Matsukuma, A.Y.; Mence, C.F.M.; Mirack, C.P.; Pilmartins, E.M.F.; Matsukuma, A.Y.; Mence, C.F.; Marthors: A; Verson, A.J.; Callada, M.; Teuhako, M.H.; Vallada, H.; Van Sluya, M.A.; Verson, V.S.; Vertore, A.L.; Zanda, M.A.; Verson, A.J.; Callada, S.; Vertore, A.L.; Zanda, M.A.; Verson, A.J.; Callada, M.A.; Verson, C.J.; A. Verson, A.J.; Zanda, A.D.; Zanda
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A;Cross-references: UNIPROT:O17412; EMBL:AF026492; NID:g2564720; PID:g2564721; PIDN:AAB8
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chitinase (EC 3.2.1.14) - yellow fever mosquito
chitinase (EC 3.2.1.14) - yellow fever mosquito)
c;Species: Aedes aegypti (yellow fever mosquito)
c;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14075
R;de la Vega, H.; Specht, C.A.; Liu, Y.; Robbins, P.W.
Insect Mol. Biol. 7, 233-239, 1997
                                         Gaps
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Insect Mol. Biol. 7, 233-239, 1997
Affitle: Chitinases are a multi-gene family in Aedes, Anopheles, and
A;Reference number: 217872
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A;Gene: CHT2
A;Introns: 462/3; 524/3; 618/1; 951/3; 1151/2
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.0%; Score 33; DB 2; Le 83.3%; Pred. No. 2.5e+02; live 1; Mismatches 0;
   Pred. No. 1.2e+02;
1; Mismatches 1
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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      71.48;
Similarity 71.4
5; Conservative
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                                                                                                                                       313 HRPLELC 319
                                                                                             2 HRPLDKC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        497 GHRPVD 502
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les 5; Conserv
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Best Local Similarity
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C, Genetics:
A, Gene: XF1640
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   Best Local
Matches
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RESULT 40
by1305
hypothetical protein TP0608 - syphilis spirochete
c; Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
c; Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
c; Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
c; Accession: B71305
R; Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDc revo, J.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A; Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A; Reference number: A71250; MUID:98332770; PMID:9665876
R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. Nature 406, 477-483, 2000
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A; A; Reference number: A82035; MUID:20406833; PMID:10952301
A; Accession: B8226
A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Cossidues: 1-189 <-HEI>
A; Cross-references: UNIRROT: Q9XTC7; GB: AE004179; GB: AE003852; NID: G9655432; PIDN: AAF9413
A; Cross-references: UNIRROT: A; A; Cross-references: UNIRROT: A; Cross-references: A; Cross-references: A; Cross-references: A; Cross-references: A; Cross-references: Cross-references: Cross-references: A; Cross-references: Cross-references: A; Cross-references: Cross-references
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Rosea: 1-296 <COL>
A;Cross-references: UNIPROT:083617; GB:AE001235; GB:AE000520; NID:g3322893; PIDN:AAC6558
A;Experimental source: strain Nichols
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Pred. No. 75;
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C;Superfamily: syphilis spirochete hypothetical protein TP0608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 57.1%; Pred. No. 75;
Matches 4; Conservative 2; Mismatches
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1612378 Total number of hits satisfying chosen parameters:

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2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Q99fx0 human papil	P02677 canis famil	P02675 homo sapien	Q9lfml arabidopsis	Q7vsa4 bordetella	Q7wq76 bordetella	Q7wc72 bordetella	Q8pkd6 xanthomonas		Q940zl arabidopsis	Q9ln43 arabidopsis	Q8mwq3 plasmodium			Q9e8g2 porcine ade		Q8rup6 oryza sativ	Q7xc43 oryza sativ	Q9ay56 oryza sativ	Q6ddt4 xenopus lae	Q6dfg8 xenopus tro		Q9pff7 xylella fas		Q9va50 drosophila	Q6ygz6 caenorhabdi	Q7jpe9 caenorhabdi	Q09937 caenorhabdi	Q86gi9 caenorhabdi	Q7jpf0 caenorhabdi	Q9si49 arabidopsis
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575 2 096989 591 1 YD72 MYCPN 58 2 QBMVTZ 159 2 QBEG4 159 2 QBEG4 201 2 Q92X9 238 2 QMTW3 240 2 QBMJP7 260 2	GUMENTS 377 AA. d) equence updat mnotation upd ge; Papilloma analysis of a ned by an ove s; IEA. ctor activity A replication, anscription, anscription,	O%; Score 42; DB 2; O%; Pred. No. 9.6; Pred. No. 9.6; Pred. 1; Mismatches 1 FRT; 31 AA. FRAT; 31 AA. Sequence update) ast annotation update) Contains: Fibrinopeptide
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DISULFIDE BONDS
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Krajewski T., Blomback B.;
Krajewski T., Blomback B.;
"The location of tyrosine-O-sulphate in fibrinopeptides.";
Acta Chem. Scand. 22:1339-1346(1968).
-!- FUNCTION: Fibrinogen has a double function: yielding monomers that polymerize into fibrin and acting as a cofactor in platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains (alpha, beta and gamma), linked to each other by disulfide bonds. PTM: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopetides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot.
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                                                                             MEDLINE=76081726; PubMed=1198547; DOI=10.1016/0049-3848(75)90106-1; Birken S., Wilner G.D., Canfield R.B.; Birken S., Wilner G.D., Canfield R.B.; "Studies of the structure of canine fibrinogen."; Thromb. Res. 7:599-610(1975).
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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InterPro; DFR00181; Fibrinogen C.
InterPro; DFR05181; Fibrinogen C.
PR0517E; PS00514; Fibrinogen C DOWAIN; PARTIAL.
Blood coagulation; Direct protein sequencing; Plasma; Sulfation.
Blood coagulation; Direct Protein Sequencing; Plasma; Sulfation.

1 19 Fibrinogen beta chain.
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01-JUL-1993 (Rel. 26, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Fibrinogen beta chain precursor [Contains: Fibrinopeptide B]
  Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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Pred. No. 1.2;
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MEDLINE=91344740; PubMed=2102623;
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Fibrinogen, thrombosis, coagulation and fibrinolysis, pp.39-48, Plenum
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MEDLINE=87146483; PubMed=3029722;
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"Studies on fibrinopeptides from primates.";
Acta Chem. Scand. 19:1788-1789(1965).
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Q9LFM1
   REFERENCE OF THE SERVICE OF THE SERV
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Liu C.Y., Koehn J.A., Morgan P.J.;
"Characterization of fibrinogen New York 1. A dysfunctional fibrinogen
with a deletion of B beta(9-72) corresponding exactly to exon 2 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99175089; PubMed=10074346; DOI=10.1021/bi982626w;
Bverse S.J., Spraggon G., Vecrapandian L., Doolittle R.F.;
"Conformational changes in fragments D and double-D from human fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";
Biochemistry 38:2941-2946(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERACTION WITH FBLN1.
MEDLINE-55370284; PubMed=7642629; DOI=10.1074/jbc.270.33.19458;
Tran H., Tanaka A., Litvinovich S.V., Medved L.V., Haudenschild C.C.,
Argraves W.S.;
"The interaction of fibulin-1 with fibrinogen. A potential role in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92340664; PubMed=1634610;
Koopman J., Haverkate F., Lord S.T., Grimbergen J., Mannucci P.M.;
"Molecular basis of fibrinogen Naples associated with defective
thrombin binding and thrombophilia. Homozygous substitution of B beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 164-491.
MEDLINE=98292395; PubMed=9628725; DOI=10.1021/bi9804129;
Everse S.J., Spraggon G., Veerappandian L., Riley M., Doolittle R.F.;
"Crystal structure of fragment double-D from human fibrin with two
different bound ligands.";
Biochemistry 37:8637-8642(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Koopman J., Haverkate F., Grimbergen J., Engesser L., Novakova I., Keret A.P. J.A., Lord S.T.,
"Abnormal fibrinogens Inmiden (B beta Arg14-->Cys) and Nijmegen (B beta Arg44-->Cys) form disulfide-linked fibrinogen-albumin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-91208409; PubMed-2018836;
Yoshida N., Wada H., Morita K., Hirata H., Matsuda M., Yamazumi
Asakura S., Shirakawa S.;
                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 164-491.
MEDLINE=97472408; PubMed=933323; DOI=10.1038/38947;
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"Crystal structures of fragment D from human fibrinogen and its crosslinked counterpart from fibrin.";
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                            REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.
MEDLINE=84305751; PubMed=6383194;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    studies of fibrinogen Baltimore II.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     replacement of B beta glycine-15 by cysteine.";
Blood 77:1958-1963(1991).
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MEDLINE=92228809; PubMed=1565641;
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                                                                                           Doolittle R.F.;
"Fibrinogen and fibrin.";
Annu. Rev. Biochem. 53:195-229(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hemostasis and thrombosis.";
J. Biol. Chem. 270:19458-19464(1995).
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J. Clin. Invest. 90:238-244(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                      Nature 389:455-462(1997).
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Lander E.S.; "Characterization of single-nucleotide polymorphisms in coding regions
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                                                                                      MEDLINE=99318093; PubMed=10391209; DOI=10.1038/10290; Cargill M., Altshuler D., Ireland J., SALar P., Ardlie K., Patil N., Shaw N., Lane C.R., Lim E.P., Kalyannarman N., Nemesh J., Ziaugra L., Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N., Shaw N., Lane C.R., Lim B.P., Kalyanaraman N., Nemesh J., Ziaugra L., Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
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Spermatophyta; Magnoliophyta; erreptocyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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MEDLINE=21361164; PubMed=11468164; DOI=10.1182/blood.V98.3.661;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20129589; PubMed=10666208; Duga S., Asselta R., Santagostino E., Zeinali S., Simonic T., Malcovati M., Manucci P.M., Tenchini M.L.; M., Manucci P.M., Tenchini M.L.; Missense mutations in the human beta fibrinogen gene cause c
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Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (UTL-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (UTL-2000) to the EMBL/GenBank/DDBJ databases.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004672; F:protein Kinase activity; IEA.
GO; GO:0006468; P:protein kinase activity; IEA.
InterPro; IPR000719; Prot_kinase.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein F2111_250.
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Arabidopsis thaliana (Mouse-ear cress).
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                                                              GLU-2; LEU-265 AND LYS-478.
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Biol. Chem. 260:4390-4396(1985)
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SEOUENCE 182 AA; ?
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                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=10545957;
                                                                                                                                                                                                                                                                                         human geneв.
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NCBI_TaxID=519;
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STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;

MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

A marxis D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

A decreno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,

A chtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

A chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

A chillingworth T., Gollins M., Cronin A., Davis P., Doggett J.,

A chillingworth T., Gollins M., Cronin A., Davis P., Doggett J.,

A chillingworth T., Gollins M., Cronin A., Davis P., Doggett J.,

A chillingworth T., Gollins M., Cronin A., Davis P., Doggett J.,

A chillingworth T., Gollins M., Sanders H., Holroyd S., Jagels K.,

Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

Rabbinowitsch E., Rutter S., Sanders M., Sauders D., Seeger K.,

Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

Unwin L., Whitehead S., Barrell B.G., Maskell D.J.,

"Comparative analysis of the genome sequences of Bordetella pertussis,

"A comparative analysis of the genome sequences of Bordetella pertussis,

"A comparative analysis and Bordetella bronchiseptica.";
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
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OrderedLocusNames=BB0456,
Borderedla bronchiseptica (Alcaligenes bronchisepticus).
Bacteria, Proceobacteria, Betaproteobacteria, Burkholderiales,
Alcaligenaceae, Bordetella.
                          Score 40; DB 2; Length 182;
Pred. No. 11;
1; Mismatches 1; Indels
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Pred. No. 15;
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Complete protecome; DNA-binding; Transcription;
Transcription regulation.
SEQUENCE 246 AA; 26265 MW; A3060D263DE488F6 CRC64;
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                        80.0%;
75.0%;
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                                                                                                                                                                   175 GHRDMDKC 182
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Query Match
Best Local Similarity
6; Conserv
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                                                                                                                        1 GHRPLDKC
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Q7VSA4;
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MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

A Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R., Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L., A Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A., A Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I., Chilingworth T., Gollins M., Cronin A., Davis P., Doggett J., Chilingworth T., Gollen A., Hamlin N., Hauser H., Holroyd S., Jagels K., Reltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K., Rabbinowitsch B., Norberczak H., O'Neil S., Ormond D., Price C., Rabbinowitsch B., Rutter S., Sanders M., Sauders M., Seguares S., Stevens K., Sharp S., Simondis M., Skelton J., Squares S., Stevens K., Sharp S., Simondis M., Skelton J., Squares S., Stevens K., Unwin L., Whitchead S., Barrell B.G., Maskell D.J.;

Bordetella parapertussis and Bordetella bronchiseptica.",
                                                                                                                  Parkhill J., Sebaina M., Preston A., Murphy L.D., Thomson N.R., Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L., Cerdenor-Tarraga A.-M., Temple L., James K.D., Harris B., Quall M.A., Achtman M., Akkin R., Baker S., Basham D., Bason N., Cherevach I., Chillingworth T., Collins M., Cronin A., Davis P., Doggett J., Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K., Leather S., Moule S., Norberzzak H., O'Neil S., Ormond D., Price C., Rabbinowitsch E., Norberzzak H., O'Neil S., Ormond D., Price C., Rabbinowitsch E., Simmondes M., Skelton J., Squares R., Squares S., Stevens K., Unwin L., Whitehead S., Barrell B.G., Maskell D.J.; Programmer Comparative analysis of the genome sequences of Bordetella pertussis, Morderella parapertussis, and Bordetella bronchiseptica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nat. Genet. 35:32-40(2003).

BMBL; BX640438; CAE30955.1; -
GO, GO:0003677; P:DNA binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR005471; HTH IClR.
InterPro; IPR009658; Wing_hlx_DNA_bnd.
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GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent, IEA.
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Alcaligenaceae, Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 80.0%; Score 40; DB 2; Length 246; Local Similarity 87.5%; Pred. No. 15; length 246; Nes 7; Conservative 0; Mismatches 1; Indels
SEQUENCE FROM N.A.
STRAIN-RB50 / ATCC BAA-588;
MEDLINE-22827954; PubMed=12910271; DOI=10.1038/ng1227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 AA; 26266 MW; 0B62039C5A55F0EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27270 MW; CF6B59887A9A962A CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Probable transcriptional regulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256 AA.
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InterPro; IPR009058; Wing_hlx_DNA_bnd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01614; IclR; 1.
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SEQUENCE 246 AA;
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Q940Z1
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                                               Gaps
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                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=152794;
                  DB 2; Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 39, DB 2; Length 135;
Pred. No. 13;
3; Mismatches 0; Indels
                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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                                                                                                                                                                                                                                       (TrEMBLrel. 22, Last sequence update) (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Putative ankyrin repeat-containing protein.
                                                                                                                                                                                        135 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219 AA
              Score 40; DB
Pred. No. 16;
0; Mismatches
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                                                                                                                                                                                                                                                                                                    Xanthomonas axonopodis (pv. citri).
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AE011861; AAM37092.1; -.
                                                                                                                                                                                                                                                                   Hypothetical protein XAC2239.
OrderedLocusNames=XAC2239;
              80.0%;
87.5%;
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62.5%;
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01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2004 (TrEMBLrel. 26.
Query Match
Best Local Similarity 87.5-
7; Conservative
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Best Local Similarity 62.5
المالية 5; Conservative
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                                                                                                                                                                                       PRELIMINARY;
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                                                                                                         139 GGRPLDKC 146
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GHKPLEEC 86
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                                                                           1 GHRPLDKC
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                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=92829;
                                                                                                                                                                                                                      01-OCT-2002
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01-OCT-2002
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Q8FP29;
                                                                                                                                                                                       OBPKD6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature
                                                                                                                                                       RESULT 8
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Gaps
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
4x1949520/R18014 36.
Arabidopsis thal Lana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II, Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
Whyyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Sacou M.,
Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                               "Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium efficiens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C., Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.K., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.K., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu G., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura E.
Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
Gojobori T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 266;
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Pfam; PF01535; PPR; 6.
TIGRFAMB; TIGR00756; PPR; 4.
TIGREAMB; TAGE AA; 29615 MW; 46CB125C324A8A30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome. - SEQUENCE 219 AA; 23415 MW; 3A6CB06E3FD59E28 CRC64;
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PROSITE; PS50297; ANK REP REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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InterPro; IPR008940; Prenyl_trans.
                                                                                                                                                                                                                                  Genome Res. 13:1572-1579(2003).
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                                                                                                                                                                                                                                                              EMBL; AP005220; BAC18771.1;
HSSP; P25963; 11KN.
                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00023; Ank; 3.
PRINTS; PR01415; ANKYRIN.
SMART; SM00248; ANK; 3.
                                                                                                                                                                                                                                                                                                                               InterPro; IPR002110; ANK.
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GHRPVNRC 50
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tes 5; Conserv
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Best Local Similarity
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Matches

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"A sub-family of common and highly conserved Plasmodium falciparum var
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=22072568; PubMed=12076777; DOI=10.1016/S0166-6851(02)00080-4;
Salanti A., Jensen A.T.R., Zornig H.D., Staalsoe T., Joergensen L.,
Nielsen M.A., Khattab A., Arnot D.E., Klinkert M.Q., Hviid L.,
Theander T.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21927235; PubMed=11930336;
Rowe J.A., Kyes S.A., Rogerson S.J., Babiker H.A., Raza A.;
"Identification of a conserved Plasmodium falciparum var gene
                                                                                                                                                                                                                                               Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39; DB 2; Length 3207;
Pred. No. 3.4e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3207 AA; 374119 MW; EC104D72B0866E5F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ### Property | Propert
                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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J. Infect. Dis. 185:1207-1211(2002).

EMBL, AJGOS319; CAD200867.1;

GO; GO:00055319; F:glycosaminoglycan binding; IEA.

GO; GO:0009405; P:pathogenesis; IEA.

InterPro; IPR006025; PEPE, M. Zn. BS.

InterPro; IPR004258; PFEMF.

PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
      PRT; 3207 AA
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                                                                                                                                                       Erythrocyte membrane protein 1 (Fragment)
                            Q8MWQ3;
01-OCT-2002 (TERMLrel. 22, Created)
01-OCT-2002 (TERMLrel. 22, Last seq
01-MAR-2004 (TERMLrel. 26, Last amm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.0%;
85.7%;
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Matches 6; Conservative
      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                   Plasmodium falciparum.
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                                                                                                                                                                                                                                                                           NCBI_TaxID=5833;
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NON TER
SEQUENCE
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Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
Theologis A., Ecker J.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C., Shinn P., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A.,
      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsia thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.
Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
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      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ecker J.R.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                        725 AA.
1; Mismatches
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Matches 6; Conservative
6; Conservative
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GHKPDDKC 103
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                                                        1 CHRPLDKC 8
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OULN43

OULN43

OU - OC

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RESULT 12 Q8MWQ3

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Gaps

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Science 300:1566-1569(2003)
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Matches 6; Conservative
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44 HRPLDTC 50
                         2 HRPLDKC 8
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OBRUP6
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Q7XDX0
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MEDLINE=20416365; PubMed=10958982; DOI=10.1016/S0168-1702(00)00157-X;
Tuboly T., Nagy E.;
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                                                                                                                                                                                                                                                                                                                                                 Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus
NCBI_TaxID=45370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence analysis and deletion of porcine adenovirus serotype 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tuboly T., Nagy E.; "Sequence analysis and deletion of porcine adenovirus serotype 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nagy M., Nagy E., Tuboly T.;
"Sequence analysis of porcine adenovirus serotype 5 fibre gene:
evidence for recombination.";
Virus Genes 34.181-185(2002).
EMBL; AF186621; AAG10229.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=HNP-61;
MEDLINE=22012773; PubMed=12018710; DOI=10.1023/A:1014580802250;
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Score 39; DB 2; Length 3287;
Pred. No. 3.5e+02;
0; Mismatches 1; Indels
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Pred. No. 7.4;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF186622; AAG10234.1; -. SEQUENCE 50 AA; 5589 MW; 02DDECC59A16F3F0 CRC64;
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Last sequence update)
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Last annotation update)
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   78.0%;
85.7%;
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85.7%;
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
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                     Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity
Local 6; Conserve
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                                                                             2 HRPLDKC 8
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=45370;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             region.";
   Query Match
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Q9E8F8
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09862
AC 098862
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DT 01-MA
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SEQUENCE FROM N.A.

PubMed=12447438; DOI=10.1038/nature01184;
Sasaki T., Matsumoto T., Yanamoto K., Sakata K., Baba T., Katayose Y.,
Sasaki T., Matsumoto T., Yanamoto K., Antonio B.A., Kanamori H.,
HOSOKawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
Ikeno M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
P0703B11.15 protein (P0485B12.7 protein).
Name=P0703B11.15; Synonyms=P0485B12.7;
Oryza sativa (japonica cultivar-group).
Bukaryota, viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaa.
                                                                                                                                                                                                                             Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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Gramene, Q7XDX0; -.
GO; GO:0003735; F:structural constituent of ribosome; IEA.
InterPro; IPR008966; Adhes bact.
InterPro; IPR008912; JUF635.
Pfam; PF04827; DUF635; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.0%; Score 38; DB 2; Length 308; 75.0%; Pred. No. 48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Rice Chromosome 10 Sequencing Consortium; "In-depth view of structure, activity, and evolution of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan (
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AE017100; AAPS4021.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 308 AA; 35289 MW; 66961D35FFE71788 CRC64;
                                                                                                                          annotation update)
                                                                                 Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         401 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
Q7XDX0;
01-0CT-2003 (TEMBLrel. 25, Created)
01-0CT-2003 (TEMBLrel. 25, Last sequence
01-MAR-2004 (TEMBLrel. 26, Last annotatic
Contains similarity to ribosomal protein.
ORFNames-OSJNBa0076M18.6;
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Name=OSJNBa0027P10.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopodinae; Xenopus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apex2-prov protein.
Name=apex2-prov;
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                                                                              SEQUENCE FROM N.A.
                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                        1 GHRPLDKC
                                                                                                                                                                                                     Gramene; Q9AY56;
                                                        NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                  Q6DDT4
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Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M., Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K, Shibata M., Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K., Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K., Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Bun M.Y., Yano M., Jiang J., Gojobori T.;

"The genome sequence and structure of rice chromosome 1.";

BMBL, AP003302, BAB85296.1; -.

EMBL, AP003302, BAB86417.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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EMBL, AE017120, AAP55032.1; -.
                                                                                                                                                                  Score.38; DB 2; Length 401;
Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.0%; Score 38; DB 2; Length 513; 75.0%; Pred. No. 81;
                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           The Rice Chromosome 10 Sequencing Consortium; "In-depth view of structure, activity, and evolution of
                                                                                                                                 Pfam; PF04827; DUF635; 1.
SEQUENCE 401 AA; 46131 MW; 9BF7BA7748970E05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEOUENCE 513 AA; 57948 MW; C9EE96E9ABA816BB CRC64;
                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein OSJNBa0027P10.13.
                                                                                                                                                                                                                                                                                        513 AA
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                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                             Created)
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InterPro; IPR008966; Adhes bact.
InterPro; IPR006912; DUF635.
                                                                                                                                                                  76.0%;
75.0%;
                                                                                                                     InterPro; IPR006912; DUF635.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 300:1566-1569(2003)
                                                                                                                                                       Query Match
Best Local Similarity 75.۰۰
امات 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 75.0
                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                 120 GHSPLOKC 127
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                                                                                                                                                                                                             1 GHRPLDKC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GHRPLDKC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=39947;
                                                                                                              Gramene; Q8RUP6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromosome 10
                                                                                                                                             SEQUENCE
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Q9AY56;
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X PubMed=12477932, DOI=10.1073/pnas.242603899;

A Riausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Strausberg R.L., Feingold E.A., Grouse L.H., Schaler G.D.,

Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heigh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshlyuki S., Carninio P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
                                                                                                                                                                                                                                                                                 Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Hsiao J., Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E., Craven B., Khalak H., Feldblyum T.V., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Oryza sativa (Rice).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Enrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUB-Kidney;
MEDLINE-22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagmer L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetic and genomic tools for Xenopus research: The NIH Xenopus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 76.0%; Score 38; DB 2; Length 513; Best Local Similarity 75.0%; Pred. No. 81; Matches 6; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC084763; AAG60187.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 513 AA; 57948 MW; C9EE96E9ABA816BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    517 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR008966; Adhes bact.
InterPro; IPR006912; DUF635.
Pfam; PF04827; DUF635; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dev. Dyn. 225:384-391(2002).
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Kiein S., Gerhard D.S.; Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases. Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases. EMBL; BCO76676; AAH76676.1; EMBL/GenBank/DDBJ databases. GO; GO:0004519; Fendonuclease activity; IEA. GO; GO:0006281; P:nNA repair; IEA. InterPro; IPR0000997; APendonucleal. InterPro; IPR000808; ExoIII xth. InterPro; IPR005135; Exo endo_phos. InterPro; IPR016665; ZF-GRR. FEam; PF03372; REA. GRR; I. FEAM; PF03372; REA. GRR; I.
                                                                                                                                                                                                                                                                                                                                                                  TIGRFAMS; TIGRO0633; xth; 1.
PROSITE; PS00726; AP NUCLEASE F1 1; 1.
SEQUENCE 517 AA; 57351 MW; 57B2062D0ED9D27F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76.0%;
75.0%;
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Best Local Similarity 75.0°,
Best G, Conservative
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                                FROM N.A.
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Matches
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X Pubmed=12477932; DOI=10.1073/pnas.242603899;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Klausner R.D., Collins F.S., Duetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hishe F.,

A Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Scapleron M., Soares M.B., Bonaldo M.F., Casnavant T.L., Scheetz T.E.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Robak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

R. Richards S., Worley D.M., Sodergren B.J., Lu X., Gibbs R.A.,

A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

A Whiting M. Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinki M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

P. A. A. A. A. A., Schein J.E.,

RA Krzywinki M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.0%; Score 38; DB 2; Length 517; 85.7%; Pred. No. 82;
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                                                                                                                                                                                                                                                         TISSUE-Kidney;
Klein S., Gerhard D.S.;
Klein S., Gerhard D.S.;
Submitted (UUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC077433; AAH77433.1; -.
GO; GO:0004519; P:endonuclease activity; IEA.
GO; GO:0006281; P:DNA repair; IEA.
InterPro; IPR000097; APendonclea.
InterPro; IPR00135; ExoIII xth.
InterPro; IPR00135; ExoIII xth.
InterPro; IPR00135; ExoGnGo_phos.
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PROSITE; PS00726; AP NUCLEASE F1 1; 1.
SEQUENCE 517 AA; 57726 MW; 92C457CB579EC530 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF03372; Exo endo phos; 1. Pfam; PF06839; zf-GRF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.
Proc. Natl. Acad. Sci. U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=apex2-prov;
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Q6DFQ8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (japonica cultivar-group).
Wkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeee, Oryza.
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. Match 76.0%; Score 38; DB 2; Length 517; Local Similarity 85.7%; Pred. No. 82; les 6; Conservative 0; Mismatches 1; Indels
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Pred. No. 99;
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626 AA; 71611 MW; C8B6FE7F24438418 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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01-WAR-2004 (TrEMBLrel. 26, Last and
Hypothetical protein OSJNBa0093113.9.
Name-OSJNBa0093113.9;
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01-OCT-2000 (TrEMBLrel. 15, Created)
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RESULT 25
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STRAINNE-20365717; PubMed=10910347; DOI=10.1038/35018003;
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ALVATENDRAG. L.M. C., Arruda P., Abreu F.A., Acencio M.,
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A colauto N.B., Colombo C., Costa M.C.R., Costa N.C.R., Costa-Neco C.M.,
Coutinho L.L., Cristofani M. Dias-Neto E. Doceas C. El-Dorry H.,
A Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
A Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
A Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
A Goldman G.H., Junqueira M.L., Kemper E.L., Kitajima J.P.,
A Krieger J.B., Kurames E.E., Lanbais M.R., Leite L.C.C.,
Lemos E.G.M., Lemos M.V.F., Lopes G.R., Lopes C.R., Marchado J.A.,
Marques M.V., Martins E.A.L., Martins E.M.F., Marcinc C.L.,
Mandado M.A., Madeira A.M.S., Nadeira H.N.F., Marcinc C.E.S.,
Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
A de Oliveira M.C. de Oliveira R.C., Palmieri D.A., Paris A.,
A de Stava A.C., de Sa R.G., Santelli R.V., Sawasaki H.E.,
A da Silva A.C., de Sa R.G., Santelli R.V., Sawasaki H.E.,
A da Silva A.C., Terenzi M.F., Truffiel S.N., Terbaro M.H.,
A de Souza A.P., Terenzi M.F., Truffiel S.N., Terbaro M.H.,
A de Souza A.P., Terenzi M.F., Truffiel S.N., Terbaro M.H.,
A de Souza A.P., Terenzi M.F., Truffiel S.N., Vettore A.L.,
A de Souza A.P., Terenzi M.F., Truffiel S.N., Terbaro M.H.,
A de Souza A.P., Terenzi M.F., Truffiel S.N., Vettore A.L.,
A de Souza A.P., Terenzi M.F., Truffiel S.N., Vettore A.L.,
A de Souza A.P., Terenzi M.F., Silva R.S., Silva R.B.,
A de Souza A.P., Terenzi M.F., Truffiel S.N., Vettore A.L.,
A de Souza A.P., Terenzi M.F., Truffiel S.N., Vettore A.L.,
A de Souza A.P., Terenzi M.F., Silva R.S., Silva R.S.,
A de Souza A.P., Terenzi M.F., Truffiel S.N., Vettore A.L.,
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Ol-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein OJ1138_B05.110.
Name-OJ1138_B05.110.
Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The genome sequence of the plant pathogen Xylella fastidiosa.";
Nature 406:151-159(2000)
                                                                                                  Xylella fastidiosa.
Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales,
Xanthomonadaceae, Xylella.
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Pred. No. 19;
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Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005486; BAC16191.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome; Hypothetical protein.
SEQUENCE 82 AA; 9067 MW; BCDE6C81A85EA7ED CRC64;
01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Last sequence update)
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75.0%;
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                                                                               OrderedLocusNames=Xf0702;
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                                                  Hypothetical protein.
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Q8H2P3
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RECORDACTE FORM N.A.

Addams M.D. Celnikers S.E., Holt R.A., Farans C.A., Gocapus J.D.,

RAMAGER M.D. Celnikers S.E., Holt R.A., Farans C.A., Gocapus J.D.,

RAMAGER M.D. Celnikers S.E., Holt R.A., Farans C.A., Gocapus J.D.,

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Burtis R.C., Gabriellan A.E., Garz C., Ferriers S., Plakson B.C.,

RAMEL D. Bolcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

Borkova D., Bolcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RAMEL D. Bolasser K.,

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RAMEL D. B., Bolasser K.,

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RAMEL D. B., Bolasser K.,

RAMEL D. B., Molasser R., Bolasser K.,

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Ramer K.M., Moy M. Wurphy E., Murphy L., Murphy D., Murphy E.,

Ramer K., Spradling A.C., Stapleton M., Studs R., Sun E.,

Syriekas R., Tector C., Turner E., Wann B.,

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Shen E.C., Shan M., Pittenn G. Y., Weinschan B.,

Ramer S.M., Woodager W., Weinschoff G.M., Weissenbach J.,

Ramer S.M., Wassarman D.A., Weinschoff S.,

Ramer S.M., Were B.W., Rolson W.,
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MEDLINE-22426065; PubMed=12537568;
Celiniker S.B., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
                                                                                                                                                                                                                                        Gaps
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidaa; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                             DB 2; Length 279;
                                                                                                                                                                                                                                        Indels
Gramene, Q8H2P3; -.
Hypothetical protein.
SEQUENCE 279 AA; 29739 MW; FEA28B9FE8AC748D CRC64;
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                                                                                                                                                     74.0%; Score 37; DB 75.0%; Pred. No. 68; ive 1; Mismatches
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                                                                                                                                                         Query Match
Best Local Similarity
Matches 6; Conserv
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"The sequence of C. e
Submitted (JUN-1995)
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Submitted (MAY-2003)
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Best Local Similarity
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                                                                                                                                                                                                                                                                      MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
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MiSTA S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Mistas S., Crosby M.A., Mungall C.J., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirakas R., Tabor P.E., Wan K., Staplecon M., Sutton G.G., Venter Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M., "Finishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence."; of the Drosophila genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lewis S.E.;
"Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Figure 1. Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.

Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.

EMBL: AR003774. AAF57073.2.

FlyBase, F8970051015; PH4-alpha-PV.

GO: GO: 0016706; F: exidoreductase activity, acting on paired do. GO: 00105738; P: protein metabolism; IRA.

InterPro; IPR006620; Pro-4-hyd_alph.

Ffam; PP03171; 200-FeII Oxy:

SMART; SMO0702; P44: 4.6606 MW; 09330C64B0769P05 CRC64;
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Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY150829; AAN75511.1; -.
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                     a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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Best Local Similarity
6; Conserve
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GHRPLEK 26
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06/025
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05-JTL-2004 (TrEMBLrel. 27, Created)
05-JTL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
K (Potassium) voltage-gated sensory channel subunit protein 1, isoform
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Rhabditidae; Peloderinae; Caenorhabditis.
                                        complex; IEA. activity; IEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
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to the EMBL/GenBank/DDBJ databases.
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Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ion transport; Ionic channel; Transmembrane; Transport
SEQUENCE 477 AA; 53396 MW; 05FASDP39C58B292 CRC64;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0008076; C:voltege-gated potassium channel com
GO; GO:0005249; P:voltege-gated potassium channel act.
GO; GO:0006812; P:voltege-gated potassium channel act.
GO; GO:0006813; P:voltege-gated potassium channel act.
InterPro; IPR001821; P:potassium ion transport; IEA.
InterPro; IPR001822; K-channel.
InterPro; IPR001822; K-channel.
InterPro; IPR0018961; Ko, Channel.
InterPro; IPR0018961; Ko, Channel.
InterPro; IPR001891; K, Channel.
InterPro; IPR001891; K, tetra.
InterPro; IPR001891; K, tetra.
InterPro; IPR00181; K, tetra.
InterPro; IPR00181; K, tetra.
InterPro; IPR00181; K, tetra.
InterPro; IPR01891; KV9CHANNEL.
PRINTS; PR01491; KV9CHANNEL.
PRINTS; PR01491; KVCHANNEL.
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Pred. No. 1.2e+02;
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MEDLINE=99069613; PubMed=9851916;
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Caenorhabditis elegans.
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Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
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PIR; T15829; T15829.
HSSP; Q54397; 1BL8.
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                                     STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                        SEQUENCE FROM N.A.
                                                                                SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                          SEQUENCE FROM N.A.
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01-JUN-2003
                                                                                                        Wilson R.;
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Q86GI9
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Matches
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
K (Potassium) voltage-gated sensory channel subunit protein 1, isoform
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                              Notitional Control of the EMBL/GenBank/DDBJ databases.

Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; U28734; AAR30209.1; -.

WormBep; C379.32, CE36242; kvs-1.

WormPep; C379.32; CE36283.

GO: GO:0016020; C:membrane; IEA.

GO; GO:0008076; C:voltage-gated potassium channel activity; IEA.

GO; GO:0006812; P:cation transport; IEA.

GO; GO:0006812; P:cation transport; IEA.

GO; GO:0006812; P:potranella civity; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37; DB 2; Length 477;
Pred. No. 1.2e+02;
0; Mismatches 1; Indels
                                   to the EMBL/GenBank/DDBJ databases.
                                                                                  Wilson R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                      Ion transport; Ionic channel; Transmembrane; Transport.
SEQUENCE 477 AA; 53428 MW; 336CCDCF6D610C22 CRC64;
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STRAIN=Bristol N2;
Bentley D.;
"The sequence of C. elegans cosmid C53C9.";
                                                                                                                                                                                                                                                        InterPro; IPR005821; Ion trans.
InterPro; IPR001622; K+channel_pore.
InterPro; IPR001622; K+channel_pore.
InterPro; IPR0013971; Ky9_channel.
InterPro; IPR003901; K_channel.
InterPro; IPR00301; K_channel.
InterPro; IPR001301; K_tetra.
InterPro; IPR001301; K_tetra.
InterPro; IPR00520; M-channel_nlg.
Pfam; PF00520; Ion_trans; I.
Pfam; PF00520; Ion_trans; I.
PRINTS; PR00169; KCHANNEL.
PRINTS; PR01494; KV9CGNANNEL.
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nes 6, Conservative
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                        Wilson R.;
Submitted (DEC-2003)
                                                                                                                           STRAIN=Bristol N2;
WormBase Consortium;
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            STRAIN=Bristol N2;
                                                                    STRAIN=Bristol N2;
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SEQUENCE FROM N.A
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                                                                               Wilson R
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Q09937
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Gaps
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R GO; GO:0016020; C:membrane; IEA.

R GO; GO:0016020; C:membrane; IEA.

R GO; GO:0005249; F:voltage-gated potassium channel complex; IEA.

R GO; GO:0006812; P:cation transport; IEA.

R GO; GO:0006812; P:cation transport; IEA.

R GO; GO:0006812; P:cation transport; IEA.

R InterPro; IPR005821; Ion trans.

R InterPro; IPR005821; Ion trans.

R InterPro; IPR003971; Kv9 channel.

R InterPro; IPR003031; K_tetra.

R InterPro; IPR003131; K_tetra.

R InterPro; IPR003131; K_tetra.

R InterPro; IPR00520; M+channel.

R InterPro; IPR00520; M+channel.

R Pfam; PP00520; IOn trans; 1.

R Pfam; PP00520; IOn trans; 1.

R Pfam; PP00520; ION trans; 1.
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Waterston R.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WormBase Consortium;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                  Wilson R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                     Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wilson R.; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wilson R.; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases
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SEQUENCE 490 AA; 54768 MW; A8346C293F93D15B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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Name=At2g14100;
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; edicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WormPep; C53C9.3b; CE30914.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.

GO; GO:0006819; F:voltage-gated potassium channel activity; IEA.

GO; GO:0006812; P:cation transport; IEA.

GO; GO:0006813; P:potassium ion transport; IEA.
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85.7%; Pred. No. 1.2e+02;
 Waterston R.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                     Wilson R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                                               Wilson R.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                    Wilson R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                             Wilson R.; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases
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SEQUENCE 495 AA; 55244 MW; 278F3635A4D83D72 CRC64;
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Last annotation update)
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InterPro; IPR001622; K+channel_pore.
InterPro; IPR001622; K+channel_pore.
InterPro; IPR003971; Kv9_channel.
InterPro; IPR00391; K_channel.
InterPro; IPR00391; K_channel.
InterPro; IPR003131; K_tetra.
InterPro; IPR003131; K_tetra.
InterPro; IPR005820; M+channel_nlg.
Pfam; PF00220; Ion_trans; 1.
Pfam; PF002214; K_tetra; 1.
PRINTS; PR001494; KV9CGRANNEL.
PRINTS; PR01491; KV9CGRANNEL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U28734; AAR25654.1; -.
WormBase; WBGene00002242; kvs-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              WormBase Consortium;
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                                                                                                                                              SEQUENCE FROM N.A. STRAIN=Bristol N2;
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                                                     SEQUENCE FROM N.A. STRAIN-Bristol N2;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
K (Potassium) voltage-gated sensory channel subunit protein 1, isoform
     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                   Caenorhabdítis elegans.
Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                GO; GO:0016021, C:integral to membrane; IEA.
GO; GO:0016076; C:voltage-gated potassium channel complex; IEA.
GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.
GO; GO:0006812; P:cation transport; IEA.
GO; GO:0006813; P:potassium ion transport; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.0%; Score 37; DB 2; Length 490; 85.7%; Pred. No. 1.2e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The sequence of C. elegans cosmid C53C9.";
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ion transport; Ionic channel; Transmembrane; Transport.
SEQUENCE 490 AA; 54737 MW; 9B362E2767CBB738 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   495 AA.
                                                                                                                                                                                                                                                                                                                           InterPro; IPR005821; Ion trans.
InterPro; IPR001622; K+channel pore.
InterPro; IPR003971; Kv9 channel.
InterPro; IPR003968; Kv Channel.
InterPro; IPR0031931; K_channel.
InterPro; IPR003131; K_tetra.
InterPro; IPR003131; K_tetra.
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MEDLINE=99069613; PubMed=9851916;
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Pfam; PF02214; K_tetra; 1.
PRINTS; PR00169; KCHANNEL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR01491; KVCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
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Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 HRPLDVC 151
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Q7JPF0
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Gaps

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Length 495;

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Lewis S.E.;
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       MEDINE-20196006; PubMed=10731132; DOI=10.1126/Science.287.5461.2185; Addams M.D., Celniker S.E., Holf R.A., Evans C.A., Gacian J.D., Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Galle R.E., Adams M.D., Celniker S.E., Holf R.A., Evans G.A., Galle R.E., Survice G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Barton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Ragers Y.H., Blazdj R.G., Champe M., Pfeiffer B.D., Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L., Abril J.F., Agbayand A., An H.J., Andrews-Pfannkoor C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Burkova D., Botchan M.R., Bouck J., Broketein P., Brottier P., Abaxter S., Dahlke C., Davenport L.B., Davies P., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J. Evangelista C.C., Ferraz C., Ferriara S., Fleischmann W., Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Abarris N.L., Harvey D., Helman T.J., Wei M.H., Ibegwam C., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
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                                         Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E., Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.-I., Carrera A.J., Creagy T.H., Buell C.R., Town C.D., Nierman W.C., Fraesr C.M., Venter J.C., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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CG3658-PA (CDC45L) (EG:BACR7A4.11 protein) (Fbgn0026143;cdc451 protein) (LD35753p).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit Fly).

Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ebhydroidea, Drosophilidae, Drosophila.

NCBI_TaxID=7227,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.0%; Score 37; DB 2; Length 518; 62.5%; Pred. No. 1.3e+02; ive 2; Mismatches 1; Indels
                                                                                                                                                                                   SEQUENCE FROM N.A.

Town C.D., Kaul S.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the cytochrome P450 family.
EMBL; AC007197; AAD25850.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        518 AA; 58814 MW; 221B94886F602F84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=CDC45L; Synonyms=EG:BACR7A4.11; ORFNames=CG3658;
                                                                                                                                                                                                                                                                                                                     GO; 0004497; F:monoxygenase activity; IEA. GO; 000418; P:electron transport; IEA. GO; 0006118; P:electron transport; IEA. InterPro; IPR001128; Cytcchrome_P450.
InterPro; IPR00128; Cytcchrome_P450.
InterPro; IPR002401; EP4501.
PRINTS; PR00463; EP4501.
PRINTS; PR00463; EP4501.
PRINTS; PR00463; EP4501.
PROSITE; PS000663; CYTCCHROME P450; UNKNOWN_1.
PROSITE; PS000663; CYTCCHROME P450; UNKNOWN_1.
PROSITE; PS000693; LUM BINDING; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 62.5
les 5; Conservative
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112 GHPPIDEC 119
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[1]
SEQUENCE FROM N.A.
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096989
AC 09698
AC 09698
DT 01-MA
DT 25-OC
DE CG365
DE CG365
CC Neopt
OC N
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Celniker S. B., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise B., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren B.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.B., Myers B.W., Gibbs R.A., Rubin G.M.; Friishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence.", Genome Biol. 3:RBSBARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99160479; PubMed=10051334;
Shaikh T.H., Gottlieb S., Sellinger B., Chen F., Roe B.A., Oakey R.J.,
Emanuel B.S., Budarf M.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Papagiannakis G., Spanos L., Bolshakov V., Siden-Kiamos I., Louis C.; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Biol. 3: RESEARCH0083-RESEARCH0083 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22426065; PubMed=12537568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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Gaps

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Edvardsen R.B., Flat M., Tewari R., Jensen M.F., Seo H.C., Lehrach H., Reinhardt R., Chourrout D.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF465689; AMM73994.1;
GO, GO:0005874; C:microtuble; IEA.
GO, GO:0005525; F:GTP binding; IEA.
GO, GO:0005525; F:GTP binding; IEA.
GO, GO:0007018; P:microtublie-based movement; IEA.
InterPro; IPR002452; Alpha_tubulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=2603 V/R / Serotype V;
MEDLINE=22222988; PubMed=12200547; DOI=10.1073/pnas.182380799;
Tettellin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S.N., Wessells M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D., Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R., Radune D., Fedorova N.B., Scanlan D., Khouri H.M., Mulligan S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Myxine glutinosa (Atlantic hagfish).
Bukaryota, Metazoa, Chordata, Craniata, Hyperotreti, Myxiniformes;
Myxinidae, Myxininae, Myxine.
      Length 591;
      Score 37; DB 1; Length 591
Pred. No. 1.5e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 58;
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 AA; 6375 MW; 0122F7B17D9D4B93 CRC64;
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                58 AA.
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR01162; ALPHATUBULIN.
      74.0%;
75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alpha-tubulin 2 (Fragment)
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Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00091; Tubulin; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                    GENPLDKC 247
                                                                                                                                    1 GHRPLDKC 8
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28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                        STRAIN=Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stapleton M., Chavez C., Dorgett V., Farfan D., Frise B., George R.,
Gonzalez M., Glarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S. E., Rubin G.M., Celniker S.,
Submitted (AUG-201) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycoplasma pneumoniae.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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                                                               Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PlyBase; FBGN0026143; CDC45L.

GO; GO:000534; C:ncytoplasm; IDA.
GO; GO:0005634; C:nccleus; IDA.
GO; GO:0005656; C:pre-replicative complex; IPI.
GO; GO:0003682; F:chromatin binding; IDA.
GO; GO:0006277; P:DNA amplification; IBP.
InterPro; IPR003874; CDC45_like.
Ffam; PP00274; CDC45; 1.
SEQUENCE 575 AA; 65890 MW; A58341D46DEFE618 CRC64;
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Pfam; PF02917; Pertussis S1; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 591 AA; 68057 MW; B958C85C9BE29B90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
05-UUL-2004 (Rel. 44, Last annotation update)
OrderedLocusNames=MPN372; ORFNames=MP464;
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Matches 6; Conservative
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                                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A
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P75409;
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Query Match

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1 CHRPLD
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                                                                                                                                                     Plasmid pSymA.
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Matches
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Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M., Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D., Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-NEW316 / Serotype III;
MEDLINE=222421698; PubMed=12354221;
Glaser P., Rusniok C., Euchrieser C., Chevalier F., Frangeul L.,
Maadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
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                                                                                                                                                           TIGR; SAG0391; -.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR002481; FUR.
InterPro; IPR009058; Wing_hlx_DNA_bnd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of Streptococcus agalactiae, a pathogen causing invasive neonatal disease.";
                                                                                   "Complete genome sequence and comparative genomic analysis of an emerging human pathogen, serotype V Streptococcus agalactiae."; Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
11-MAR-2004 (TrEMBLrel. 26, Last annotation update)
14-ypothetical protein gb80427.
0rderedLocusNames=g80427;
Streptococcus agalactiae (serotype III).
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                  159 AA; 18584 MW; 31FBA715A358C127 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD002003; FVR; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 159 AA; 18584 MW; 31FBA715A358C127 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invasive neonatal disease.";
Mol. Microbiol. 45:1499-1513(2002).
EMBL; AL766845; CAD46071.1; -.
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                                                                                                                                                                                                                                                                                 ProDom; PD002003; FUR; 1.
Complete proteome.
SEQUENCE 159 AA: 18584
                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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7 GHRPLD 12
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GHRPLD 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kunst F.;
                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Q92XY9
ID Q92XY
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MEDLINE=2136509; PubMed=11481432; DOI=10.1073/pnas.161294798;
Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
Yeh K.-C., Davis R.W., Federapiel N.A., Long S.R.;
"Nucleotide sequence and predicted functions of the entire
Sinorhizobium meliloti pSymA megaplasmid.";
Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888 (2001).
-- SIMILARITY: Contains I HHT tetR-type DNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=W83;
MEDLINE=22829867; PubMed=12949112;
DOI=10.1128/JB.185.18.5591-5601.2003;

DOI=10.1128/JB.185.18.591-5601.2003;

DOI=10.1128/JB.185.18.591-5601.2003;

Bisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
"Complete genome sequence of the oral pathogenic bacterium
Porphyromonas gingivalis strain W83.";
"Gomplete genome sequence of the oral pathogenic bacterium
Porphyromonas gingivalis strain W83.";
J. Bacteriol. 185:5591-5601(2003).

EMBL, ARQ66816.1; -.
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GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
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01-MAR 2004 (TrEMBLrel. 26, Last sequence update)
01-MAR 2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
OrderedLocusNames=P61818;
Porphyromonas gingivalis (Bacteroides gingivalis)
Bacteria, Bacteroidetes; Bacteroides; (class);
                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Length 201;
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Transcription regulation.
SEQUENCE 201 AA; 21500 MW; 447B9E9BP63EF551 CRC64;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DRA-2004 (TrEMBLrel. 26, Last annotation update)
Putative transcriptional regulator.
ORFNames=SMa2008;
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                                                                                                                                                                            Rhizobium meliloti (Sinorhizobium meliloti)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 72.0%; Score 36; DB Local Similarity 100.0%; Pred. No. 77; es 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro, IPR009057; Homeodomain_like.
InterPro, IPR001647; HTH_TetR.
Pfam; PF00440; TetR N; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 GHRPLD 180
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Search completed: June 1, 2005, 11:52:01 Job time: 122 secs
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"The genome of the natural genetic engineer Agrobacterium tumefaciens CS8.";
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
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STRAIN=CZECH II; TISSUE=Mammary tumor;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
NCBI TaxID=176299;
                                                                            72.0%; Score 36; DB 2; Length 238; 85.7%; Pred. No. 91; 1.1ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.0%; Score 36; DB 2; Length 240; 85.7%; Pred. No. 92; 1ve 0; Mismatches 1; Indels
Complete proteome; Hypothetical protein.
SEQUENCE 238 AA; 26945 MW; DCA6C728CE6C8448 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome; Hypothetical protein.
SEQUENCE 240 AA; 27768 MW; 7BABSFD4C723D616 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agrobacterium tumefaciens (strain C58 / ATCC 33970)
                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 21, Created)
(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 294:2317-2323(2001).
EMBL; AE009016; AAL41475.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein Atu0456.
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01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OrderedLocusNames=Atu0456;
                                                                                                                               Conservative
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                                                                                                       Local Similarity
tes 6; Conserv
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Name=Apex2;
                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2002
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01-JUN-2003
                                                                            Query Match
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QBUI44
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Matches
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088328
AC 08832
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DE APEXZ
GN Name=
CO Eukar
OC Eukar
OC Mamma
OC Mamma
OC RESULT
RN (1)
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Gaps
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO26769; AAH26769.1; --
HSSP, P09010; 1AKO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR005135; Exo endo phos.
Pfam; PF03372; Exo endo phos; 1.
PROSITE; PS00726; AP NUCLEASE F1 1; 1.
SEQUENCE 246 AA; 27389 MW; 194A612EF3CB1D8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:1924872; Apex2.
GO; GO:0005743; C:mitochondrial inner membrane; IDA
GO; GO:0005634; C:nucleus; IDA.
                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 72.0%; Score 36; DB Local Similarity · 71.4%; Pred. No. 95; nes 5; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                STRAIN=CZECH II; TISSUE=Mammary tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000097; APendonclsel
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201 HRPIDHC 207
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Sequence 5, Appli Sequence 28544, A Sequence 28874, A Sequence 26924, A Sequence 30324, A Sequence 22575, A Sequence 24235, A Sequence 28870, A Sequence 28870, A Sequence 283, Appl Sequence 283, Appl

52, Appl 283, App 28127, A 45137, A 6, Appli 58607, A 43265, A 2, Appli 9, Appli

Sequence Seq

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RESULT 1
US-08-058-099-10
i Sequence 10, Application US/08058699
i Patent No. 5443827
GENERAL INFORMATION:
APPLICANT: Edgar Haber
APPLICANT: Christoph Bode
TITLE OF INVENTION: THROMEN
TITLE OF INVENTION: THROMEN
INVERSE OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STREET: ABSACHUSELE
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 558X
OPERATING SYSTEM: MS-DOS (Version 5.0)
COMPUTER: WACHDERIES IN DATA:
APPLICATION NUMBER: US AS
COMPUTER: WACHDERIES IN S-DOS (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US AS
                              US-09-252-991A-26924
US-09-252-991A-2275
US-09-252-991A-30324
US-09-252-991A-28870
US-08-252-991A-28870
US-08-311-731A-52
US-08-311-731A-52
US-08-311-731A-283
US-09-252-991A-28127
US-09-270-767-45137
US-09-270-767-45137
US-09-270-767-45137
US-09-270-767-45137
US-09-270-767-43265
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                                                                                                                                                                                        US-09-637-145-2
US-09-644-827B-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PILING DATE: 1993063
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: N/A
FILING DATE: N/A
ATTORNEY/AGENT INFORMATION:
NAME: Janis K. Fraser, Ph.D.
REGISTRATION NUMBER: 34,819
REGISTRATION NUMBER: 05433/004001
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 200154
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (617) 542-5070 TELEFAX: (617) 542-8906
TYPE: AMINO ACID STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: Linear
US-08-058-699-10
 TELEFAX:
 Sequence 12, Appl
Sequence 12, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 35, Appl
Sequence 35, Appl
Sequence 9, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 4232, Ap
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Sequence 4, Appli
Sequence 9617, Ap
Sequence 9, Appli
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Sequence 11, Appl
Sequence 1, Appli
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Sequence 4, Appli
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                                                                            June 1, 2005, 11:41:40; Search time 28 Seconds (without alignments) 18.662 Million cell updates/sec
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Sequence 4, Ap
Sequence 12, A
Sequence 12, A
Sequence 12, A
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Sequence 26
Sequence 23
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'CgnZ_6/ptodata1/iaa/5A_COMB.pep:*
'CgnZ_6/ptodata1/iaa/5B_COMB.pep:*
'CgnZ_6/ptodata1/iaa/6A_COMB.pep:*
'CgnZ_6/ptodata1/iaa/6A_COMB.pep:*
'CgnZ_6/ptodata1/iaa/RB_COMB.pep:*
'CgnZ_6/ptodata1/iaa/PCTUS_COMB.pep:*
'CgnZ_6/ptodata1/iaa/backfiles1.pep:*
         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-058-699-10
US-08-058-699-11
US-08-649-51-11
US-08-448-547-1
US-08-448-547-1
US-08-448-547-1
US-08-470-152-12
US-08-470-152-12
US-08-470-152-12
US-08-470-152-12
US-08-290-853-33
US-08-290-853-35
US-08-290-853-35
US-08-290-853-35
US-08-290-853-35
US-08-290-853-35
US-08-290-133-990C-4232
US-09-213-999C-4232
US-08-206-176-4
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US-09-252-991A-23750
                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                              513545 seqs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                        - protein search, using sw model
                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                              US-09-424-940A-1
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Match Length
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Perfect score:
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Length 7; Indela

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US-10-142-915-6

US-10-142-915-6

US-10-142-915-6

Sequence 6, Application US/10142935

Sequence 6, Application US/10142935

Sequence 6, Application US/10142935

GENERAL INFORMATION:

APPLICANT: HOOK, Magnus A.O.

TITLE OF INVERTION: METHOD AND COMPOSITIONS FOR INHIBITING THROWBIN-INDUCED COAGULATIC

TITLE OF INVERTION NUMBER: US/10/142,935

CURRENT APPLICATION NUMBER: US/10/142,935

CURRENT APPLICATION NUMBER: US 60/290,072

PRIOR APPLICATION NUMBER: US 60/290,072

PRIOR PILING DATE: 2001-05-13

NUMBER OF SEQ ID NOS: 11

SEQ ID NO 6

LENGTH: 20

LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                     COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Flam Pr. Compatible
COMPUTER: PatentIn Pelease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,547
FILING DATE: 03-JUN-1995
PRIOR APPLICATION NUMBER: CT/JP94/01844
FILING DATE: 01-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-297325
FILING DATE: 02-NOV-1993
ATTORNEY/AGENT INPORMATION:
SUGHRUE, MION, ZINN, MACPEAK & SEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                         2100 Pennsylvania Avenue, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT; ORGANISM: Staphylococcus epidermidis
US-10-142-935-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: Q-3
TELECOMMUNICATION:
TELEPHONE: (202)293-7060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-448-547-1
               STREET: ALL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GHRPLDK 7
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                                                                                                                   20037
ADDRESSEE:
                                                                 STATE: D
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
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US-08-448-547-1
i Sequence 1, Application US/08448547
i Sequence 1, Application US/08448547
i Patent No. 581068
i GENERAL INFORMATION:
APPLICANT: Soe, Gilbu
APPLICANT: Inuzuka, Kimiko
APPLICANT: Ito, Yumiko
i TITLE OF INVENTION: ANTI-HUMAN SOLUBLE FIBRIN ANTIBODY,
ITLE OF INVENTION: HYBRIDOMA, AND IMMUNOASSAYING METHOD
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 41; DB 1; Length 8; Best Local Similarity 100.0%; Pred. No. 4.1e+05; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                           Sequence 11, Application US/08058699
Parent No. 5443827
GENERAL INFORMATION:
GENERAL INFORMATION:
BEGAT HABET
APPLICANT: Christoph Bode
TITLE OF INVENTION: FIBRIN-TARGETED INHIBITORS OF
TITLE OF INVENTION: THROMBIN
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 502 or 555X

OPERATING SYSTEM: MS-DOS (Version 5.0)

SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/058,699

FILING DATE: 19330503

CLASSIFICATION: 530

PILOS APPLICATION 193705

APPLICATION NUMBER: M/A

ATTONEY/AGNIT INFORMATION:

NAME: Janis K. FTASET, Ph.D.

REGISTRATION NUMBER: 34,819

REGISTRATION NUMBER: 34,819

REGISTRATION NUMBER: 34,819

REGISTRATION NUMBER: 34,819

TELEFRANCE/DOCKET NUMBER: 05433/004001

TELEPHONE: (617) 542-5070

TELEFRANCE (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: AMINO ACID STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: Linear
US-08-058-699-11
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US-08-058-699-11
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                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Dean, Richard T
APPLICANT: Buttram, Scott
APPLICANT: McBride, well lam
APPLICANT: Lister-James, John
APPLICANT: Lister-James, John
APPLICANT: Civitello, Edgar R
TITLE OF INVENTION: Technetium-99m Labeled Peptides for
TITLE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
                                                                                                              100.0%; Score 41; DB 1; Length 28; 100.0%; Pred. No. 0.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 41; DB 1; Length 28; 100.0%; Pred. No. 0.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,152
FILING DATE: 06-UJW-1995
CLASSIFICATION: 424
ATTONENY/AGENT INFORMATION:
NAME: NO. 5780007nan, Kevin B
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,205-L
TELEPOMUNICATION INFORMATION:
TELEPAK: 312-715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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; Patent No. 5922303
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                       Sequence 12, Application US/08470152
Patent No. 5780007
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELERAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                          Conservative
                       ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-486-135-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: peptide US-08-470-152-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
  amino acid
                                                                                                            Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                      1 GHRPLDK 7
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                                                                                         Sequence 4, Application US/10142935
Patent No. 683378
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DAVIS, Stacey
TITLE OF INVERTION: METHOD AND COMPOSITIONS FOR INHIBITING THROWBIN-INDUCED COAGULATI
TITLE OF INVERTION NUMBER: US/10/142,935
CURRENT APPLICATION NUMBER: US 60/290,072
PRIOR FILING DATE: 2001-05-13
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
IENGTH: 25
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APPLICANT: Buttram, Scott
APPLICANT: Buttram, Scott
APPLICANT: Buttram, Scott
APPLICANT: Givitello, Milliam
APPLICANT: Lister-James, John
APPLICANT: Lister-James, John
APPLICANT: Civitello, Edgar R
TITLE OF INVENTION: Technetium-99m Labeled Peptides for
TITLE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CONTY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 41; DB 4; Length 25; 100.0%; Pred. No. 0.09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,135
PILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: NO. 572094nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,205-N
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/08486135
Patent No. 5720934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 7; Conservative
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10 GHRPLDK 16
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15 GHRPLDK 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
US-08-486-135-12
                                                                                     10-142-935-4
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; Sequence 33, Application US/08290853
; Patent No. 5989519
; GENERAL INFORMATION:
    APPLICANT: Dean, Richard T
    APPLICANT: Buttram, Scott
    TITLE OF INVENTION: Technetium-99m Labeled Peptides for
    TITLE OF INVENTION: Technetium-99m Labeled Peptides for
    TITLE OF INVENTION: Imaging Inflammation
    NUMBER OF SEQUENCES: 37
    CORRESPONDENCE ADDRESS:
    ADDRESSE: Banner & Allegretti, Ltd.
    STREET: 10 South Wacker Drive, Suite 3000
    STREET: 10 South Wacker Drive, Suite 3000
    STREET: 10 South Wacker Drive, Suite 3000
    STREET: Banner & Allegretti, Ltd.
    STREET: 11 South Wacker Drive, Suite 3000
    STREET: 10 South Wacker US/08/290,853
    STREET: 10 South Wacker NUMBER: 35,303
    REFERENCE/DOCKET NUMBER: 35,303
    RELECHANS: 312-715-1234
    TELEPHONE: 312-715-1234
    TELEPHONE: 312-715-1234
    TELEPHONE: 312-715-1234
    TREERING SEQ ID NO: 33: SEQUENCE CHARACTERISTICS: LENGTH: 28 mmino acide
    TYPR: amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 41; DB 2; Length 28; 100.0%; Pred. No. 0.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
  PatentIn Release #1.0, Version #1.30
                                            PELICATION NUMBER: US/07/871,282A
FILING DATE: 20-APR-1992
CLASSIFICATION: 424
ATTOMNEY/AGENT INFORMATION:
NAME: MCDANIEL BY PARTICIA A.
REGISTRATION NUMBER: 33,194
REPRENCE/DOCKET NUMBER: DITI 111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (603) 437-8970
TELEPRX: (603) 437-8977
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                             not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
                           CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                            TYPE: maino acid
STRANDEDNESS: not rel
TOPOLOGY: linear
MOLECULE TYPE: peptide
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TOPOLOGY: linear
MOLECULE TYPE: peptide
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     SOFTWARE:
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US-07-871-282A-10
Sequence 10, Application US/07871282A
Sequence 10, Application US/07871282A
Fatent No. 5965107
GENERAL INFORMATION:
APPLICANT: Dean, Richard T.
APPLICANT: Buttram, Scott
APPLICANT: Lister-James, John
APPLICANT: Lister-James, John
TITLE OF INVENTION: Technetium-99m Labeled Peptides for TITLE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE Diatide, Inc.
STREET: 9 Dalta Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 41; DB 2; Length 28; 100.0%; Pred. No. 0.1;
             APPLICANT: Buttram, Scott
APPLICANT: McBride, William
APPLICANT: Lister-James, John
APPLICANT: Lister-James, John
APPLICANT: CISTER S. TITLE OF INVENTION: Technetium-99m Labeled Peptides for TITLE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 14
ADDRESSEE: Diatide, Inc.
STREET: 9 Delta Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NATA:
APPLICATION NUMBER: US/08/468,964B
FILING DATE: 06-JUN-1995
CLASSIFICATION WINBER: 33,194
REGISTRATION NUMBER: 33,194
REFERENCE/DOCKET NUMBER: DITI 111D4
TELEPHONE: (603) 437-8970
TELEPAX: (603) 437-8970
TELEPAX: (603) 437-8970
TELEPAX: (803) 437-8970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Dean, Richard T.
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: not re-
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                ZIP: 03053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                         CITY: Londonderry STATE: NH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E
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Sequence 10, Application US/08170299;
Patent No. 6086849;
GENERAL INFORMATION:
APPLICANT: Dear, Richard T
APPLICANT: Dear, William
APPLICANT: Lister-James, John
APPLICANT: Civitello, Edgar R;
TITLE OF INVENTION: Technetium-99m Labeled Peptides for TITLE OF INVENTION: Imaging;
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 41; DB 3; Length 28; 100.0%; Pred. No. 0.1;
                                                                              Sequence 10. Application US/08582134B
Patent No. 6074627
GENERAL INFORMATION:
APPLICANT: Butram, Scott
APPLICANT: McBride, William
APPLICANT: Lister-James, John
APPLICANT: Civitello, Edgar R.
TITLE OF INVENTION: TECHNETIUM-99m LABELED PEPTIDES FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/582,134B
FILING DATE: 14-MAY-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: McDaniels, Patricia A.
REGISTRATION NUMBER: 33,194
REFERENCE/DOCKET NUMBER: DITI 112D1
TELEPHONE: (603) 437-8970
TELEPHONE: (603) 437-8970
TELEFRAX: (603) 437-8970
TELEFRAX: (603) 437-8970
TELEFRAX: (603) 437-8970
TELEFRAX: (803) 437-8970
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                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Diatide, Inc.
STREET: 9 Delta Drive
CITY: Londonderry
STATE: NH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GHRPLDK 7
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US-08-170-299-10
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                                                                                                                                                                                        /label= Amide
/note= "The carboxyl terminus is modified to an
amide"
/label= BAT /note= "The amino terminus is linked to a BAT radiolabel binding moiety."
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                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 41; DB 2; Length 28; 100.0%; Pred. No. 0.1;
                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dean, Richard T.
APPLICANT: Buttram, Scott
APPLICANT: McBride, William
APPLICANT: Lister-James, John
APPLICANT: Civitello, Edgar R.
TITLE OF INVENTION: TECHNETIUM-99m LABELED PEPTIDES FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/253,678A
FILING DATE: US-094/254
ATTORNEY/AGENT INFORMATION:
CLASSIFICATION NUMBER: 33,194
REFERENCE/DOCKET NUMBER: DITI 112
TELECOMMUNICATION INFORMATION:
TELEPHONE: (603) 437-8970
TELEPAX: (603) 437-8970
TELEPAX: (603) 437-8977
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
TWATTOM TO ACIDES
TO ACIDED
TO AC
                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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US-08-253-678A-10
; Sequence 10, Application US/08253678A
; Parent No. 599784
; GENERAL INFORMATION:
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STRANDEDNESS: not relevant
                                                                                        FEATURE:

NAME/KEY: Modified-site

LOCATION: 28

CTHER INFORMATION: /label=

OTHER INFORMATION: /note=

COTHER INFORMATION: amide"

US-08-290-853-33
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Diatide, Inc.
STREET: 9 Delta Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
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Best Local Similarity 100.
Matches 7; Conservative
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MOLECULE TYPE: peptide
OTHER INFORMATION:
OTHER INFORMATION:
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of the cysteine is
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/note= "The carboxyl terminus is modified to an
amide"
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                                                                                                                            /label= Picolinoyl
/note= "The amino terminal residue is
pyridine-2-carbonyl; the thiol of the
protected by an acetamidomethyl group.
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OTHER INFORMATION: /label= Picolinoyl
OTHER INFORMATION: /note= "The amino terminal residue is
                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 41; DB 2; Length 30; 100.0%; Pred. No. 0.11; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:

APPLICANT: Dean, Richard T
APPLICANT: Buttram, Scott
TITLE OF INVENTION: Technetium-99m Labeled Peptides for TITLE OF INVENTION: Technetium-99m Labeled Peptides for TITLE OF INVENTION: Imaging Inflammation
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PAIR PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,535
FILING DATE: 07-UN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: No. 5711931nan, Kevin E
REGISTRATION NUMBER: 35,303
REPERNICH/DOCKET NUMBER: 92,112-J
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/08472535 Patent No. 5711931
                                                                                                        LOCATION: 1..3
OTHER INPORMATION: /label:
OTHER INFORMATION: pyridin
OTHER INFORMATION: pyridin
OTHER INFORMATION: protect
FRATURE:
NAME/KEY: Modified-site
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INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                       NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100...
Tr Conservative
                                           MOLECULE TYPE: peptide
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OTHER INFORMATION:
OTHER INFORMATION:
    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 10 South
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                       linear
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                       TOPOLOGY:
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                                                                                                                                                                                                                                                          LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 35, Application US/08290853
Patent No. 5989519
GENERAL INFORMATION: Richard T
APPLICANT: Buttram, Scott
TITLE OF INVENTION: Technetium-99m Labeled Peptides for TITLE OF INVENTION: Imaging Inflammation
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/170,299
FILING DATE: 09-FEB-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6086849nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,205-H
TELECOMUNICATION INFORMATION:
TELEPANS: 312-715-100
TELEFAX: 312-715-100
TELEFAX: 312-715-100
TELEFAX: 312-715-100
TELEX: 910-21-5317
INPORMATION POR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acide

"TONE AND ADDRESSION OF SEGUENCE CHARACTERISTICS:
"TONE AND ADDRESSION OF SEGUENCE CHARACTERISTICS:
LENGTH: 28 amino acide
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NAME: No. 5989519nan, Kevin E
REGISTRATION NUMBER: 35,303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION
TELEPHONE: 312-715-1000
TELEPAX: 312-715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear;
MOLECULE TYPE: peptide
US-08-170-299-10
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1 GHRPLDK 7
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US-08-290-853-35
COUNTRY:
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US-08-266-178A-9
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OTHER INFORMATION: /label= Picolinoyl
OTHER INFORMATION: /note= "The amino terminal residue is
OTHER INFORMATION: pyridine-2-carbonyl; the thiol of the cysteine
OTHER INFORMATION: residue is protected by an acetoamidomethyl
  pyridine-2-carbonyl; the thiol of the cysteine residue is protected by an acetoamidomethyl
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                                                                                           100.0%; Score 41; DB 1; Length 31; 100.0%; Pred. No. 0.11; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/08484774

Patent No. 5807538
GENERAL INFORMATION:
APPLICANT: Dean, Richard T
APPLICANT: Lees, Robert S.
APPLICANT: Buttram, Scott
TITLE OF INVENTION: Technetium-99m Labeled Peptides for TITLE OF INVENTION: Imaging Inflammation
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER RELABBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORRANTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,774
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 5807538nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,112-K
TELECOMMUNICATION INFORMATION:
TELEFUNDE: 312-715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: 111inois
CUNTRY: USA
ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPAX: 312-715-1234
TELEX: 910-221-3317
INPORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Modified-site LOCATION: 1..3
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                                                                                                                Local Similarity 100.
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) OTHER INFORMATION:

) OTHER INFORMATION:

US-08-472-535-9
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Best Local Similarity
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US-08-484-774-9
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                                                                                             Query Match
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Matches
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Sequence 4322, Application US/09513999C
Fatent No. 6783961
GENERAL INFORMATION:
APPLICANT: Ducas Milne Edwards, J.B.
APPLICANT: Ducas Gordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
PLIE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT APPLICATION DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 1..3

CTHER INFORMATION: /label= Picolinoyl
OTHER INFORMATION: /note= "The amino terminal residue is
OTHER INFORMATION: pyridine-2-carbonyl; the thiol of the cysteine
OTHER INFORMATION: residue is protected by an acetoamidomethyl
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Sequence 9, Application US/08266178A
Patent No. 6017510
GENERAL INFORMATION:
APPLICANT: Dean, Richard T
APPLICANT: Buttram, Scott
TITLE OF INVENTION: Technetium-99m Labeled Peptides for TITLE OF INVENTION: Imaging Inflammation
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDERSS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/266,178A
FILING DATE: 27-JUN-1994
CLASSIPICATION: 435
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PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: NO. 6017510nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,112
TELEPHONE: 312-715-1000
TELEPHONE: 312-715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPAX: 312-12-17
TELEFAX: 910-221-5317
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                     STREET: 10 South
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
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US-09-513-999C-4232
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RESULT 17

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Query Match
Best Local Similarity 100.
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Best Local Similarity 100.
Matches 7; Conservative
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ZIP: 98105
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US-08-206-176-4
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US-09-919-033
US-09-919-039-33
Sequence 33, Application US/09919039
Patent No. 6727066
GENERAL INFORMATION:
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REPERROR: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT APPLICATION NUMBER: 00/09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
NUMBER: OF SEQ ID NOS: 401
SEQ ID NO 33
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FILE REFERENCE: 59.US2.REG CURRENT APPLICATION NUMBER: US 60/122,487
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 4231
LENGHH: 150
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                                                                                                                                                                                                                                                                 LOCATION: -30..-1

THEN INFORMATION: SCORE 12.2

OTHER INFORMATION: Seq LLLLLLCVFLVKS/QG
US-09-513-999C-4232
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; OTHER INFORMATION: SCORE 12.2
; OTHER INFORMATION: SEQ LLLLLLCVFLVKS/QG
US-09-513-999C-4231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 19
US-09-513-999C-4231
Sequence 4231, Application US/09513999C
Fatent No. 6783961
GENERAL INFORMATION:
GENERAL INFORMATION:
FAPLICATION:
FAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 7; Conservative
                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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45 GHRPLDK 51
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SOFTWARE: Patent.pm
SEQ ID NO 4232
LENGTH: 118
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LOCATION: -30..-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Garner, Ian
APPLICANT: Dalrymple, Michael A
APPLICANT: Prunkard, Donna E
APPLICANT: Foster, Donnald C
TITLE OF INVENTION: Production of Fibrinogen in Transgenic
TITLE OF INVENTION: Animals
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 41; DB 1; Length 491; 100.0%; Pred. No. 2.1; ive 0; Mismatches 0; Indels
                                                                                                                                                        100.0%; Score 41; DB 4; Length 488; 100.0%; Pred. No. 2.1;
                                                                                                                                                                                                   0; Indels
TYPE: PRT
ORGANISM: Homo sapiens
FRATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6727066 3393861CD1
US-09-919-039-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
COMFUTER: Patem: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/206,176
                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 93-15
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9617, Application US/09949016
Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: ZymoGenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08206176
Patent No. 5639940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JONGTH: 491 amino acids
TYPE: amino acid
TOPOLOGY: linear
J. MOLECULE TYPE: protein
US-08-206-176-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
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APPLICANT: DAVIS, Stacey
APPLICANT: HOOK, Magnus A.O.
TITLE OP INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATIC
FILE REFERENCE: P07201US01/BAS
CURRENT APPLICATION NUMBER: US/10/142,935
CURRENT FILING DATE: 2002-05-13
PRIOR PILING DATE: 2001-05-13
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 5:
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 26425, Application US/09248796A

Sequence 26415, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION:

TITLE OF INVENTION:

FILE REPERENCE: 107196-132

CURRENT FILING DATE: 1999-02-12

CURRENT FILING DATE: 1999-02-13

PRIOR FILING DATE: 1999-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 26425

LENGTH: 74
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                                                                                                                                                                     DB 4; Length 15; 0.55;
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                                                                                                                                                                                                                0; Indels
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                                                                                                                                                                   87.8%; Score 36; DB 100.0%; Pred. No. 0.5 tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36; ; Pred. No.
                                                                                  ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-142-935-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                        US-10-142-935-5
; Sequence 5, Application US/10142935
; Patent No. 6835378
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100.0%;
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85.7%;
                      SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 15
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ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                6; Conservative
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NUMBER OF SEQ ID NOS: 11
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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US-09-248-796A-26425
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US-10-142-935-9

i Sequence 9, Application US/10142935

j Sequence 9, Application US/10142935

general information:
APPLICANT: DATE, Stacey
APPLICANT: BOXE, Magnus A.O.
TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATI
FILE REFERENCE: P072-011801/Bas.
CURRENT PILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: US/10/142,935
PRIOR APPLICATION NUMBER: US 60/290,072

PRIOR APPLICATION DATE: 2001-05-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/10142935

Sequence 8, Application US/10142935

Patent No. 6835378

GENERAL INPORMATION:
APPLICANT: DAVIS, Stacey
APPLICANT: HOCK, Magnus A.O.
APPLICANT: HOCK, Magnus A.O.
CURRENT APPLICATION NUMBER: US/10/142,935

CURRENT APPLICATION NUMBER: US/10/142,935

CURRENT APPLICATION NUMBER: US 60/290,072

PRIOR FILING DATE: 2001-05-13

PRIOR FILING DATE: 2001-05-13
             APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

RICHARDY FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , ORGANISM: Staphylococcus epidermidis
US-10-142-935-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 10
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                              US-09-949-016-9617
                                                                                                                                                                                                                                                                                                                         SEQ ID NO 9617
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US-10-142-935-8
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GENERAL INFORMATION:
APPLICANT:
MARC J. Rubenfield et al.
TITLE OF INVENTION:
MACC J. Rubenfield et al.
TITLE OF INVENTION:
MACC J. REBURGENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION:
MACC J. REPUBLENCE:
MACC J. REPUBLENCE:
MACC J. REPUBLENCE:
MACC J. REPUBLENCE:
MACC J. RELATING TO SET AND THERAPEUTICS
TITLE OF INVENTION:
MACC J. REPUBLENCE:
MACC J. REPUBLE:

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Patent No. 6551795
GENERAL INFORMATION:
FOR INVENTION:
TITLE OF INVENTION:
APPLICANT:
RIBERERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR REPLING DATE: 1999-02-18
PRIOR REPLING DATE: 1999-02-18
PRIOR REPLING DATE: 1999-07-18
PRIOR SPLING DATE: 1999-07-18
PRIOR SPLING DATE: 1999-07-18
PRIOR SPLING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 25874
LENGTH: 305
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
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Pred. No. 55;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28544
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Similarity 71.4%;
5; Conservative ;
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Best Local Similarity 71.4%;
Matches 5; Conservative
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261 GHQPLDQ 267
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Matches 5; Conserv
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US-09-252-991A-26924
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                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERCHOINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERCHOINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23750
LENGTH: 194
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Sequence 5, Application US/09799875

Sequence 5, Application US/09799875

GENERAL INFORMATION:
APPLICANT: Mayers, Rachel
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Williamson, Mark
TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses
TITLE OF INVENTION: Therefor
FILE REFERENCE: 35800/20996

CURRENT APPLICATION NUMBER: US/09/799,875

CURRENT FILING DATE: 2001-03-06

PRIOR FILING DATE: 2000-02-11

PRIOR APPLICATION NUMBER: 09/659,287

PRIOR APPLICATION NUMBER: 09/659,287

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 92;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.8%; Score 36; DB 4; Length 194;
100.0%; Pred. No. 8.3;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                           ; Sequence 23750, Application US/09252991A; Patent No. 6551795
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ORGANISM: Pseudomonas aeruginosa
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Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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US-09-799-875-5
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134 GHRPLD 139
                                                                68 GHRPADK 74
GHRPLDK 7
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                                                                                                                                                           RESULT 27
US-09-252-991A-23750
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US-09-252-991A-28544
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SOFTWARE: Fabl
SEQ ID NO 5
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US-09-799-875-5
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US-09-252-991A-28870

is Sequence 28870. Application US/09252991A

is Sequence 28870. Application US/09252991A

is Patent No. 6551795

is GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

ITILE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERABEUTICS

FILE REFERENCE: 107196.136

CURRENT RILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

iENGTH: 1020
                                                                                                                                                                                                                                                           PAGENTE OF STATES APPLICATION US/09252991A

PRETENT NO. 6551795

GENERAL INFORMATION:
APPLICANT: MAC J. Rubenfield et al.
APPLICANT: MAC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REPRENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
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Pred. No. 2e+02;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28870
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Best Local Similarity 71.4%;
Matches 5; Conservative
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                                                                                         36 GHRPADR 42
                                              GHRPLDK 7
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US-09-252-991A-30538
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
RIOR FILING DATE: 1998-02-18
RIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22575
LENGTH: 497
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Patent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                    Score 33; DB 4; Length 379;
Pred. No. 69;
1; Mismatches 1; Indels
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Pred. No. 92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22575, Application US/09252991A; Patent No. 6551795; GENERAL INFORMATION:
                                                                                                                                            TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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ORGANISM: Pseudomonas aeruginosa
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US-09-252-991A-30324
       1998-07-27
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
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PRIOR FILING DATE: 1998-07-;
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26924
LENGTH: 379
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GHRPMQK 46
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GHRPADR 91
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Best Local Similarity
Matches 5; Conserv
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US-09-252-991A-30324
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Sequence 28127, Application US/09252991A
Patent No. 6551795
BATENT NIF 6551795
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: A
                                                                                                                                                                                                 Sequence 283, Application US/08311731A
Sequence 283, Application US/08311731A
Sequence 283.6
GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: BELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF SQUENCES: 411
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
                             Gaps
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                               Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
FILING DATE:
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                             3; Mismatches
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CURRENT FILING DATE: 1999-02-18
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BER: US 60/074,788
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REPERENCE/DOCKET NUMBER: C0044
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
TELEFAX: 617/720-3441
INFORMATION FOR SEQ ID NO: 283:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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57.1%;
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amino acid
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Best Local Similarity 57.1.
                             4; Conservative
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                                                                                            246 GHRPIER 252
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283 GHRPIER 289
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                                                                   1 GHRPLDK 7
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US-09-252-991A-28127
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APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30538
LENGTH: 266
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Patent No. 6583266
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
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Pred. No. 76;
1; Mismatches 0; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
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Pred. No. 1.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REPERENCE/DOCKET NUMBER: C0044/7125
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: MYCOBACTERIUM LEPRAE
US-08-311-731A-52
                                                                                                                                                                                                                                                                                                            ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30538
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83.3%;
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57.1%;
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 83.3
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein HYPOTHETICAL: YES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 HRPLDR 194
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 HRPLDK 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 37
US-08-311-731A-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
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US-09-270-767-45137
Sequence 45137, Application US/09270767
Fatent No. 6703491
GENERAL INFORMATION:
FAPLICANT: Homburger et al.
TITLE OF INVENTION: Nuclei acids and proteins of Drosophila melanogaster:
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 45137
LENGTH: 548
                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                   Query Match 78.0%; Score 32; DB 4; Length 515; Best Local Similarity 83.3%; Pred. No. 1.5e+02; Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 78.0%; Score 32; DB 4; Length 548; Best Local Similarity 83.3%; Pred. No. 1.6e+02; Matches 5; Conservative 1; Mismatches 0; Indels
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CTHER INFORMATION: Xaa means any amino acid
US-09-270-767-45137
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ 1D NOS: 33142
; SEQ 1D NO 28127
; LENGTH: 515
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Psecudomonas aeruginosa
US-09-252-991A-28127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Drosophila melanogaster
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408 HRPLDR 413
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Search completed: June 1, 2005, 11:53:56 Job time: 29 secs

|||||: 282 GHRPLE 287

8 8

1 GHRPLD 6

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09/424940age 1 Seg. 10s 132

Nickol, G.

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

June 1, 2005, 11:37:44; Search time 112.467 Seconds (without alignments) 24.072 Million cell updates/sec Run on:

Title: Perfect score:

US-09-424-940A-1 1 GHRPLDK 7 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2105692 seqs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

2105692

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:* Database :

geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

STRAMARTES

SUMMARIES	Description	1314 Aap71314 Sequence	Aar05558	Aar65792	Aar63269	. Aap82686		5793 Aar65793 Fibrin-sp	Aar63270	9 Abb76979	1931 Aaw11931 Fibrinoge	Add32229	8629 Aar28629 N-termina	4829 Aar44829 Human fib	4838 Aar44838 Human fib	8036 Abb78036 Peptide W	0 Aar44830 Hur	Aae34816 S.	Aae34814 S.	Aar40010 SC:	Add12888	Aao18333	2547 Aar42547 Leukocyte	2546 Aar42546 Leukocyte	6240 Abp56240 Targeting	
S	ΩI	AAP7131	AAR05558	AAR65792	AAR63269	AAP82686	AAR44837	AAR65793	AAR63270	ABB7697	AAW1193	ADD32229	AAR28629	AAR44829	AAR44838	ABB78036	AAR4483	AAE34816	AAE34814	AAR40010	ADD12888	AA018333	AAR42547	AAR42546	ABP56240	
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	Length	7	7	7	7	80	80	80	80	9	10	11	12	12	12	14	16	20	25	28	28	28	29	30	30	
de	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	
	Score	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	
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30 8 ADH58575 87 4 ABB11339 140 4 AAU33273 141 4 AAU33273 141 4 AAU33273 141 4 AAU33273 142 4 AAW78493 455 8 ABM85150 474 8 ABM85150 474 8 ABM85150 474 8 ABM84481 474 8 ABM84481 474 8 ABM85151 474 8 ABM85151	Radioph Human h Human e Novel	Aac10778 Human pol AagC0150 Human sec Aam78493 Human pro Abm85159 Human dia Abm85150 Human dia Abm85150 Human dia		Aar82243 Human fib Aam78492 Human pro Aae36413 Human FBG Add69271 Human fib Add69272 Human fib
07000000000000000000000000000000000000	ADH58575 ABB11339 AAG00151 AAU33273	AAO10778 AAG00150 AAM78493 ABM85149 ABM85150 ABM85152	ABM84478 ABM84481 ABM84482 ABM85151 ADE76868	AAR82243 AAM78492 AAE36413 ADD69271 ADD69272
	30 8 87 4 1118 3	4 6 4 8 8 8	4 4 4 4 8 8 8 8 8 8	24977
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44444444444444444444444444444444444444	26 27 29	2	36 33 40 40	14444 122 1244 13

ALIGNMENTS

Sequence of fibrin immunogen for the prepn. of monoclonal antibodies (MAbs) . Fibrin-specific monoclonal antibody; screening Location/Qualifiers AAP71314 standard; peptide; 7 AA. /label= Lys-OH (revised)
(revised)
(first entry) Key Misc-difference 7 25-MAR-2003 03-OCT-2002 19-JUN-1991 Homo sapiens AAP71314; RESULT 1

WO8706263-A.

22-OCT-1987.

87WO-US000862. 86US-00851514. 14-APR-1987; 14-APR-1986;

(GEHO) GEN HOSPITAL CORP. (GEHO) GEN HOSPITAL CORP. (GEHO) GEN HOSPITAL CORP.

Matsueda GR, Haber E; WPI; 1987-306855/43. Screening of fibrin-specific monoclonal antibodies - by contact with immobilised crosslinked fibrin clot and screening with detectable labelling step.

Disclosure, Page 7; 41pp; English.

The MAbs are specific to fibrin without fibrinogen cross-reactivity. They have increased binding to in vitro and in vivo thrombi. The MAbs can be used in immunoasays for fibrin in the presence of fibrinogen or other proteins. They can be used as immunoaffinity ligands for the purification of fibrin. (Updated on 03-OCT-2002 to add missing OS field.) (Updated on

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Synthetic epitopic peptide(s) of variable length - capable of eliciting fibrin specific antibodies free of fibrinogen cross-reactivity.
                                                                                                                                         Fibrin-specific epitopic peptides; thrombi detection; fibrinogen; antifibrin-specific monoclonal antibodies.
                                                 AAR65792 standard; peptide; 7 AA.
                                                                                                                      Fibrin-specific epitopic peptide.
                                                                                                                                                                                                                                                     84US-00603155.
86US-00824228.
89US-00454954.
                                                                                                                                                                                                                                                                                                                Matsueda GR, Haber E;
                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                            (GEHO ) GEN HOSPITAL CORP.
                                                                                         (revised)
                                                                                                                                                                                                                                                                                                                                    WPI; 1994-332411/41
  1 GHRPLDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7 AA;
                                                                                                                                                                                                                                                              30-JAN-1986;
22-DEC-1989;
                                                                                                                                                                                                                                  24-AUG-1992;
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                                                                                       25-MAR-2003
26-JUN-1995
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21-JUL-1995
                                                                                                                                                                                           US5357042-A
                                                                                                                                                                                                               18-0CT-1994
                                                                                                                                                                        Synthetic.
                                                                      AAR65792;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                Hui K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
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                              RESULT 3
                                         AAR65792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide is epitopic to fibrin, allowing anti-fibrin Abs to be raised without cross-reactivity to fibrinogen. They are particularly useful in detection of fibrin and thrombi. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fibrin-specific monoclonal antibodies - lacking fibrinogen cross-reactivity, obtd. using peptide(s) comprising fibrin-specific epitopic
                                                           Gaps
                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 41; DB 2; Length 7; Best Local Similarity 100.0%; Pred. No. 1.8e+06; Matches 7; Conservative 0; Mismatches 0; Indels
                                     100.0%; Score 41; DB 1; Length 7; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                          fibrin; fibrinogen; thrombi; immunoaffinity.
                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                    'label= His or Pro
                                                                                                                                                                                                                                                                                                                                                                /label= Asp or Glu
                                                                                                                                                                                                                                                                                                                                                                                   /label= Lys or Arg
                                                                                                                                                                                                                                                                                                                        label= Pro or Val
                                                                                                                                                                                                                                                                                                                                            'label= Leu or Val
25-MAR-2003 to correct PA field.)
                                                                                                                                                  AAR05558 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 17; 12pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hui K;
                                                                                                                                                                                                                                                                                                                                                                                                                                              86US-00824228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84US-00603155
                                                                                                                                                                                                                       Peptide antigenic to fibrin.
                                                                                                                                                                                          (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GEHO ) GEN HOSPITAL CORP.
                                                          7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1990-185723/24.
                                     Query Match
Best Local Similarity
                                                                             CHRPLDK 7
                                                                                        Misc-difference
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                   Sequence 7 AA;
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                                                                                                                                                                                         25-MAR-2003
11-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                      US4927916-A
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                                                                                                                                                                                                                                                               Synthetic
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                                                                                                                                                                    AAR05558;
                                                          Matches
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AAR05558
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92US-00932729.

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                                      AAR65789-R65794 are synthetic peptides comprising fibrin-specific epitopic sequences, they can be used to prepare hybridoma cell lines, which produce antifibrin-specific monoclonal antibodies substantially devoid of fibrinogen cross-reactivity. These antibodies are useful in the in vivo and in vitro detection of thrombi and fibrin deposits. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibitor; thrombin; chimeric molecule; fibrin-binding; antibody; hirudin; monoclonal; 59D8; fibrinopeptide B; coagulation; P79; coronary stent implantation; adjunctive therapy; fibrinogen; haemorrhage.
                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                            Length 7;
                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beta-peptide used to raise monoclonal antibody 59D8.
                                                                                                                                                                                                                                         100.0%; Score 41; DB 2; L
100.0%; Pred. No. 1.8e+06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR63269 standard; peptide; 7 AA.
Claim 2; Col 18; 12pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                              Local Similarity 100.
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Gaps

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GHRPLDK 7

used be to PA

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New anti-human fibrin mono: clonal antibody, for diagnosing thrombosis prepd. from hybridoma obtd. by applying cell fusion mouse spleen and mouse myeloma-cells, and measures human fibrin.
                                                                                                                                                          The peptide is linked to a carrier protein via a linking agent and u to immunise mice. The mouse spleen cells and amyeloma cell line can fused to produce a hybridoma secreting MAbs which bind specifically human fibrin but not fibrinogen. (Updated on 25-MAR-2003 to correct field.)
                                       (MITN ) MITSUBISHI GAS CHEM CO INC
                                                                                                                                           Claim 1; Page 1; 8pp; Japanese
               86JP-00237876.
                                                               WPI; 1988-152086/22.
                                                                                                                                                                                                                                                                                    Local Similarity.
                                                                                                                                                                                                                                               Sequence 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8 AA;
              08-OCT-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JP05304992-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
AAR44837
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                                                                                                                                                                                                                                                                                           This sequence represents beta-peptide which was used to raise the monoclonal antibody 5998. The antibody binds fibrin and may be used in the chimeric molecule of the invention. The chimeric molecule further comprises a thrombin inhibitor linked to the fibrin-binding antibody through a covalent linkage. The chimeric molecule allows fibrin-specific antibody targetting of hirudin and other thrombin inhibtors, which is more potent than thrombin on its own. The epitope to which 5908 binds becomes available only after thrombin cleaves fibrinopeptide B. The chimeric protein may be used for preventing coagulation of the blood. Anti-thrombin targetting can be esp. useful in highly thrombogenic situations such as coronary stent implantation and can be used as an adjunctive therapy with highly selective thrombolytic agents. The thrombin inhibitor is localised to sites of thrombin activity by the antibody which binds to thrombin but does not cross react with uncleaved fibrinogen. The selectivity of inhibition allows the total amount of thrombin inhibitor used to be substantially reduced, resulting in a coronary process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                   Fibrin-binding antibody linked to thrombin inhibitor - useful for preventing blood coagulation by specifically targetting inhibitor to site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fibrin; beta chain; N-terminal; monoclonal antibody; thrombosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 41; DB 2; Length 7; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human fibrin beta chain N-terminal.
                                                                                                                                                                                                                                                                      Example 1; Page 13; 53pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP82686 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86JP-00237876.
                                                                           94WO-US004881
                                                                                                   93US-00058699
                                                                                                                                                                   Runge M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
(first entry)
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                                                                                                                          (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  correct PN field.)
                                                                                                                                                                                                                                              of thrombin activity.
                                                                                                                                                                                           WPI; 1994-358195/44.
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                                                                                                                                          (UYEM-) UNIV EMORY
                                                                                                                                                                  Haber E, Bode C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7 AA;
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                         W09425491-A1
                                                                           03-MAY-1994;
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                                                  10-NOV-1994.
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05-DEC-1990
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 Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue plasminogen activator; t-PA; mutein; fibrin; antigen; anti-fibrin; monoclonal antibody; hybridoma; thrombolysis antithrombotic agent; bispecific antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hybrid monoclonal antibody - used for prepn. of thrombolytic having drug increased thrombolytic activity and specificity and reduced reactivity to fibrinogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human fibrin beta-chain peptides A and B were synthesised and coupled to BSA for injection into mice. The peptides were used to raise antibodies to human fibrin. Monoclonal antibodies specific for fibrin are used in the production of bispecific amonoclonal antibodies which also recognise truncated tPA muteins lacking the finger, EGF and Kringle I domains
                                                                    Gaps
                                                                    ;
0
100.0%; Score 41; DB 1; Length 8; 100.0%; Pred. No. 1.8e+06; rive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human fibrin beta-chain N-terminal peptide A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 14; 38pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                           AAR44837 standard; peptide; 8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-JUN-1994 (first entry)
                                                                    7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1993-408334/51.
                                                                                                                                                                          1 GHRPLDK 7
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us-09-424-940a-1.rag

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This sequence represents a synthetic beta-peptide which was used to immunopurify the monoclonal antibody 59D8 which was raised against beta-peptide (see also AAR63569). The antibody binds fibrin and may be used in the chimmeric molecule of the invention. The chimmeric molecule further comprises a thrombin inhibitor linked to the fibrin-binding antibody through a covalent linkage. The chimmeric molecule allows fibrin-specific antibody targetting of hirudin and other thrombin inhibitors, which is more potent than thrombin on its own. The epitope to which 59D8 binds becomes available only after thrombin cleaves fibrinopeptide B. The chimmeric protein may be used for preventing coagulation of the blood. Anti-thrombin targetting can be esp. useful in highly thrombogenic situations such as coronary stent implantation and can be used as an ediunctive therapy with highly selective thrombolytic agents. The chrombin inhibitor is localised to sites of thrombin activity by the artibody which binds to thrombin but does not cross react with uncleaved fibrinogen. The selectivity of inhibition allows the total amount of thrombin inhibitor used to be substantially reduced, resulting in a reduced potential for generalised haemorrhaging. (Updated on 25-MAR-2003) to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preventing blood coagulation by specifically targetting inhibitor to site of thrombin activity.
                                                                                                                                                                Inhibitor; thrombin; chimeric molecule; fibrin-binding; antibody; hirudin; monoclonal; 59D8; fibrinopeptide B; coagulation; P79; coronary stent implantation; adjunctive therapy; fibrinogen; haemorrhage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fibrin-binding antibody linked to thrombin inhibitor - useful for
                                                                                                                      Synthetic beta-peptide used to raise monoclonal antibody 59D8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 41; DB 2; Length 8; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 14; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB76979 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    93US-00058699
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                                                (revised)
(first entry)
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1994-358195/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYEM-) UNIV EMORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GHRPLDK 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bode C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8 AA;
                                                                                                                                                                                                                                                                                                            WO9425491-A1
                                                                                                                                                                                                                                                                                                                                                                                                    03-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-MAY-1993;
                                                25-MAR-2003
21-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-JUL-2002
                                                                                                                                                                                                                                                                                                                                                           10-NOV-1994
                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haber E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB76979;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
ABB76979
                             셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR65789-R65794 are synthetic peptides comprising fibrin-specific epitopic sequences, they can be used to prepare hybridoma cell lines, which produce antifibrin-specific monoclonal antibodies substantially devoid of fibrinogen cross-reactivity. These antibodies are useful in the in vivo and in vitro detection of thrombi and fibrin deposits. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic epitopic peptide(s) of variable length - capable of eliciting fibrin specific antibodies free of fibrinogen cross-reactivity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note='"May be absent and if present may be bonded to keyhole limpet hemocyanin."
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fibrin-specific epitopic peptides; thrombi detection; fibrinogen; antifibrin-specific monoclonal antibodies.
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                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 41; DB 2; Length 8; 100.0%; Pred. No. 1.8e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                     Pred. No. 1.8e+06;
                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
100.0%; FI
                                                                                                                                                                                                                                                                                                                                                                                                                       Fibrin-specific epitopic peptide.
                                                                                                                                                                                                                                                       AAR65793 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR63270 standard; peptide; 8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84US-00603155.
86US-00824228.
89US-00454954.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haber E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92US-00932729
                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                     Similarity 100 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Conservative
                                                                                                                                                                                                                                                                                                                                                        (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matsueda GR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1994-332411/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GHRPLDK 7
                                                                                                                         GHRPLDK
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                                                                                         GHRPLDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8 AA;
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30-JAN-1986;
22-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
26-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-0CT-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                        AAR65793;
                     Best Local
Matches
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                                                                                                                                                                                                                               AAR65793

110 AAR6

20 AAR6

XX AAR6

XX AAR6

XX AAR6

XX Fibb

XX Fibb

XX AAR6

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ID AAR6
XX
AC AAR6
                                                                                                                                                                                                         RESULT 7
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Gaps

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Residues 45-54 of human fibrinogen beta chain precursor.

AAR63270;

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WPI; 1995-206667/27.
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                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                         7
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1 GHRPLDK 7
                                                                                                                                                                                                                        1 GHRPLDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                JS2003109431-A1
                                                                                                                                                                   Sequence 10 AA;
                                                                                                                                                  coagulation
                                                                                                                                                                                                                                                                                                                           15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                          ADD32229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith TH;
                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                      RESULT 11
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                                                                                                                                                                                                                                        polypeptide derived from all or part of the alpha- or beta-chains of fibrin by substitution of at least one arginine residue by Cit. The Cit containing polypeptides can be used for in vitro diagnosis of rheumatoid polyarthritis (RP), by detecting disease-specific autoantibodies, and therapeutically for neutralising the RP-associated autoimmune response. The present sequence is a fragment (residues 45-54) of the human fibrinogen beta chain precursor, which was used in an example from the
                                                                                                                                                                                  New citrulline-containing polypeptide from fibrin, useful for diagnosis and treatment of rheumatoid polyarthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monoclonal; antibody; human; soluble; fibrin; fibrinogen; urea-treated; des-AABB; A-alpha-chain; immunoassay; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                Gaps
        anti-inflammatory; fibrin; rheumatoid polyarthritis;
                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                               The present invention relates to a citrulline (Cit) containing
                                                                                                                                                                                                                                                                                                                                             Length 9;
                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                            100.0%; Score 41; DB 4; I
100.0%; Pred. No. 1.8e+06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fibrinogen A-alpha-chain residues 17-26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disseminated intravascular coagulation.
                                                                                                                            (UYTO-) UNIV TOULOUSE SABATIER PAUL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kohno I, Inuzuka K, Ito Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW11931 standard; peptide; 10 AA
                                                                                                                                                                                                             Example 1; Page 12; 23pp; French
                                                                                          99FR-00008470.
                                                                                                           99FR-00008470
                 human; fibrinogen beta chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94WO-JP001844
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                                                                                                                                                                                                                                                                                                                                                               7; Conservative
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                                                                                                                                              Serre G, Sebbag M;
                                                                                                                                                                 WPI; 2001-114394/13
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 GHRPLDK 7
                                                                                                                                                                                                                                                                                                                                                                                GHRPLDK
                                                                                                                                                                                                                                                                                                                          Sequence 9 AA;
                                                    FR2795735-A1
                                    Homo sapiens
                                                                                         01-JUL-1999;
                                                                                                          01-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9512617-A1
                                                                       05-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-MAY-1995.
                                                                                                                                                                                                                                                                                                         invention
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                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
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proinflammatory; tetrapeptide; inflammation; synovial joint inflammation;
rheumatoid arthritis; fibrinogen A alpha chain; fibrin polymerisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention describes a method of inducing proinflammatory effects in synovial or fibroblast cells comprising exposing the cells to a specific teraspeptide (GPRP) peptide (I). (I) is used for inducing proinflammatory effects in synovial or fibroblast cells. An analogue of (I) is used for treating or preventing inflammation of a synovial joint or rheumatoid arthritis in a subject. (I) is used to identify a receptor for (I) comprising exposing several fibroblastic cells or synovial cells to (I).
                                                                                                                                                                                                                                                        not with human fibrinogen. Specifically when the MAb reacts with ureatreated des-AABB fibrin the reaction is not inhibited by peptides corresponding to fibrinogen A-alpha-chain residues 17-26 (AAW11931), B-beta-chain residues 15-24 (AAW11932) or gamma-chain residues 312-324 (AAW11933). The MAb is useful in immunoassays for solubbe fibrin in plasma samples (e.g. by sandwich immunoassay), particularly for the diagnosis of pathological conditions such as disseminated intravascular
                                                                                                                                                                                                                        A novel monoclonal antibody (MAb) reacts with human soluble fibrin, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inducing proinflammatory effects in human synovial or fibroblast cells comprises using a specific tetrapeptide which can also identify a receptor to the tetrapeptide.
Monoclonal antibody reactive with soluble human fibrin - but not with fibrinogen, is useful for fibrin immunoassay in plasma specimens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biotinylated fibrin polymerisation associated control peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 2; Length 10;
Pred: No. 0.029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                Example 3; Page 15; 32pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADD32229 standard; peptide; 11 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
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WPI; 1993-408334/51.
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUN-1991;
                                                                                                                                                                                                    20-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fibrinogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                        AAR44829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR44838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
                                        AAR44829
                                                                                                       $\times \times \
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bi:specific antibody useful for treating thrombotic obstructive diseases e.g. cardiac infrarction - comprises antihrombus antibody variable region and anti-thrombolytic substance antibody variable region with no heavy, chain constant region domains 2 and 3.
(I) Can identify, isolate and clone the cell receptor to which it binds. This is the amino acid sequence of a control peptide associated with the ihlbition of fibrin polymerisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents an N-terminal peptide of human fibrin. It was used in the production of bispecific monoclonal antibodies which are specific for fibrins, but do not bind fibrinogen, and and are specific for anti-thrombolytic substance. The compsn. contg. these Abs lacks the side effects of prior art Ab targetted thrombolytic agents and has enhanced thrombolytic activity. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bispecific hybrid monoclonal antibody; thrombolytic agent;
cardiac infarction; arterial embolism; cerebral infarction;
peripheral arterial/venous obstruction; retinal arterial obstruction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                 100.0%; Score 41; DB 7; Length 11; 100.0%; Pred. No. 0.032;
                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Watanabe A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 3; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR28629 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-terminal human fibrin peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91JP-00112874.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                        Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kurokawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1992-383677/47.
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                                                                                                                                                                                                                                                                                                                            1 GHRPLDK 7
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                        GHRPLDK
                                                                                                                                     Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12 AA;
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22-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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13-MAR-1992;
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                                                                                                                                                                                                    Query Match
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AAR28629

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AC AAR28

DT 25-MA
DT 22-MA
DT 22
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                                                                                                                                                                                                               Tissue plasminogen activator; t-PA; mutein; fibrin; antigen; anti-fibrin; monoclonal antibody; hybridoma; thrombolysis antithrombotic agent; bispecific antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hybrid monoclonal antibody - used for prepn. of thrombolytic having drug increased thrombolytic activity and specificity and reduced reactivity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue plasminogen activator; t-PA; mutein; fibrin; antigen; anti-fibrin; monoclonal antibody; hybridoma; thrombolysis antithrombotic agent; bispecific antibody.
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                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. .11
/note= "human fibrin beta-chain residues 1-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 41; DB 2; Length 12; llarity 100.0%; Pred. No. 0.036; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "BSA carrier is attached to Cys"
                                                                                                                                                            Human fibrin beta-chain N-terminal peptide (1-11)-Cys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 9; 38pp; Japanese.
AAR44829 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human fibrin beta-chain peptide B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR44838 standard; peptide; 12 AA.
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                                                                                                          (first entry)
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The specification describes peptides which correspond to portions of fibrin/fibrinogen beta chain sequencés, and act as modulators of fibrin fibrinogen beta chain sequencés, and act as modulators of fibrin E activity, and in turn modulators of fibrin E effects. Such effects include induction of call proliferation, angiogenesis fibrogenesis and collagen synthesis. The peptides are used for wound heart muscle or limb replacement surgery. They are also used for treating ischaemia, reduction of scarring, and prevention of restenosis. The peptides may also be used for treating atherogenesis, rheumatoid carribritis, diabetes, renal disease, psoriassis, macular degeneration, or cancer. The peptides are also useful for modifying fibrin glues, and may be incorporated into a stent which is introduced into the arteries of the
                                                                                                                                                                                                                                                               patient during an angioplasty procedure for preventing restenosis. BAB78036-3-38 represent peptides derived from fibrin/fibrinogen beta chain sequences. The peptides are derived from the region where plasmin cleaves the molecule, and contain a Ceterminal Cys which does not appear in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue plasminogen activator; t-PA; mutein; fibrin; antigen; anti-fibrin; monoclonal antibody; hybridoma; thrombolysis antithrombotic agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         monoclonal antibody - used for prepn. of thrombolytic having drug sed thrombolytic activity and specificity and reduced reactivity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human fibrin internal peptide fragment was identified as a candidate immunogen to raise antibodies to human fibrin. Monoclonal antibodies specific for fibrin are used in the production of bispecific monoclonal antibodies which also recognise truncated tPA muteins lacking the finger, EGF and Kringle 1 domains
                                                                                                                                                                                                                                                                                                                                                                                                     Length 14;
                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 5; Length 13.
Pred. No. 0.043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human fibrin beta-chain internal peptide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR44830 standard; peptide; 16 AA.
                                Example 3; Page 46; 84pp; English
                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1993-408334/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bispecific antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                    wild type protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GHRPLDK
                                                                                                                                                                                                                                                                                                                                                                     Sequence 14 AA;
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 psoriasis
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Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 16
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                                                                                                                                                                                                                Hybrid monoclonal antibody - used for prepn. of thrombolytic having drug increased thrombolytic activity and specificity and reduced reactivity to
                                                                                                                                                                                                                                                                                                            Human fibrin beta-chain peptides A and B were synthesised and coupled to BSA for injection into mice. The peptides were used to raise antibodies to human fibrin. Monoclonal antibodies specific for fibrin are used in the production of bispecific monoclonal antibodies which also recognise truncated tPA muteins lacking the finger, EGF and Kringle I domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel peptides acting as modulators of fibrin fragment E activity for treating disease responding to stimulation or inhibition of cell proliferation or angiogenesis e.g. wound healing, ischemia, cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fibrin beta chain; fibrinogen beta chain; fibrin fragment E; cell proliferation; angiogenesis; fibrogenesis; collagen synthesis; wound healing; skin graft; heart muscle revascularisation; linb replacement; ischaemia; scarring; restenosis; atherogenesis; rheumatoid arthritis; diabetes; renal disease; psoriasis; macular degeneration; cancer; fibrin glue; stent; angioplasty; antennapedia protein; membrane translocation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                    reatch 100.0%; Score 41; DB 2; Length 12; Local Similarity 100.0%; Pred. No. 0.036; es 7; Conservative 0; Mismatcher.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide WTM250 derived from fibrin/fibrinogen beta chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stirk CM;
                                                                                                                                                                                                                                                                                Example 1; Page 14; 38pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB78036 standard; peptide; 14 AA
                                                                                                              91JP-00148936
                                                                                 92JP-00158301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-DEC-2000; 2000GB-00030309
                                                                                                                                               TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                Hybrid monoclonal antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYAB-) UNIV ABERDEEN
                                                                                                                                                                               WPI; 1993-408334/51
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6 GHRPLDK 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GHRPLDK
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12 AA;
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               JP05304992-A
                                                                             17-JUN-1992;
                                                                                                              20-JUN-1991;
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                                              19-NOV-1993
                                                                                                                                                                                                                                                 fibrinogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Gaps ö

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Treating or preventing thrombin-induced coagulation of blood for treating a disease condition such as stroke, myocardial infarction, sickle-cell crisis or venous thrombosis by administering a SdrG protein.
                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method for treating or preventing thrombin-
induced cosqulation of blood by administering a SdrG protein. The method
is sued for preparing a composition for treating myocardial infarction,
stroke, sickle-cell crisis or venous thrombosis. The present sequence is
Staphylococcus epidermidis fibrinogen (Fg) Bbeta chain peptide used to
illustrate the method of the invention
                              Thrombin-induced blood coagulation; myocardial infarction; SdrG protein; sickle-cell crisis; venous thrombosis; stroke; therapy; anticoagulant;

    S. epidermidis fibrinogen (Fg) Bbeta chain peptide, betal-25.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 41; DB 6; Length 25; Best Local Similarity 100.0%; Pred. No. 0.085; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reagent; site imaging; technetium-99M labelled; peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scintigraph imaging agent specific binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR40010 standard; peptide; 28 AA.
                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Col 19; 29pp; English
                                                                                                                                                                                                                                   (TEXA ) UNIV TEXAS A & M SYSTEM
                                                                                                                                                                                                      11-MAY-2001; 2001US-0290072P.
                                                                                                                                                                          13-MAY-2002; 2002WO-US014741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92US-00871282
                                                                                     Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                         WPI; 2003-140257/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 GHRPLDK 21
                                                                                                                                                                                                                                                                Hook MAO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GHRPLDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 25 AA;
                                                          fibrinogen; Fg.
                                                                                                                    WO200292117-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9321962-A1
                                                                                                                                               21-NOV-2002.
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23-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                Davis S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR40010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating or preventing thrombin-induced coagulation of blood for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method for treating or preventing thrombin-
induced coagulation of blood by administering a SdrG protein. The method
is sued for preparing a composition for treating myocardial infarction,
stroke, sickle-cell crisis or venous thrombosis. The present sequence is
Staphylococcus epidermidis fibrinogen (Fg) Bbeta chain peptide used to
illustrate the method of the invention
                                                                                                                                                                                                                                                                                                       Thrombin-induced blood coagulation, myocardial infarction, SdrG protain, sickle-cell crisis, venous thrombosis, stroke, therapy, anticoagulant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a disease condition such as stroke, myocardial infarction, sickle-cell crisis or venous thrombosis by administering a SdrG protein.
                                                          Gaps
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                                                                                                                                                                                                                                                                          S. epidermidis fibrinogen (Fg) Bbeta chain peptide, beta6-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 41; DB 6; Length 20; 100.0%; Pred. No. 0.065; tive 0; Mismatches 0; Indels
                           100.0%; Score 41; DB 2; Length 16; 100.0%; Pred. No. 0.05;
                                                         0; Indels
                                                          0; Mismatches
                                                                                                                                                                                       AAE34816 standard; peptide; 20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE34814 standard; peptide; 25 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Col 19; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TEXA ) UNIV TEXAS A & M SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-MAY-2002; 2002WO-US014741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-MAY-2001; 2001US-0290072P
                                                                                                                                                                                                                                                                                                                                                                Staphylococcus epidermidis.
                                                                                                                                                                                                                                                 28-MAY-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                       Best_Local Similarity 100
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
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GHRPLDK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-140257/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hook MAO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 GHRPLDK 16
                                                                                     GHRPLDK 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GHRPLDK 7
Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                       sickle-cell cri
fibrinogen; Fg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                             WO200292117-A1
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                                                                                                                                                                                                                    AAE34816;
                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Davis S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 18
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ID AAE3
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AC AAE3
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RESULT 21
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                                                                                                               The sequence is that of a specific binding peptide used as part of a reagent for preparing a scintigraphic imaging agent for imaging sites within a mammalian body. In this the peptide is covalently linked to a radiolabel-binding moiety which is capable of forming a complex with a radiolsotope, pref. technetium-99M. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention describes a reagent (A) for producing an agent for imaging sites in a mammal comprising a specific binding peptide (I) of 3-100 amino acids and, covalently linked to the side chain of an amino acid, residue in (I), a radiolabel binding group (II). Also new are (I) scintigraphic imaging agents (SIA) containing (A) in which (II) is bound to a radiolabel; (2) kits for preparation of a radiopharmaceutical comprising (A) and enough reducing agent to label (A) with Technetium-99m. Depending on the nature of (I), SIA can be used to image e.g:

    contg. technetium-

                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scintigraphic imaging agent comprising specific binding peptide - attached via an amino acid side chain to a radio:label binding gp. provides rapid imaging of tumours, thrombosis etc.
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                                                                                                                                                                                                                                      ;
0
                       Civitello
                                                                                                                                                                                                                                                                                                                                                                                                                    imaging; scintigraphic imaging agent; SIA; Technetium-99m; somatostatin receptor; leukocytes; atherosclerotic plaque; deep vein thrombosis.
                                                                                                                                                                                                               100.0%; Score 41; DB 2; Length 28; 100.0%; Pred. No. 0.097;
                                                                                                                                                                                                                                    0; Indels
                                                              Reagents for preparing scintigraphic imaging agents 99M labelled peptide(s) contg. 3-100 aminoacid(s).
                                                                                                                                                                                                                                                                                                                                                                                                scintigraphic imaging agent associated peptide #12
                      Lister-James J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lister-James J,
                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                 ADD12888 standard; peptide; 28 AA
                   Mcbride W,
                                                                                            Claim 35; Page 39; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mcbride W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 14; Page 34; 43pp; English
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                                                                                                                                                                                                                        Local Similarity 100.
                   Dean RT, Buttram S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Buttram S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-039983/04.
 (DIAT-) DIATECH INC
                                          WPI; 1993-368429/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIAT-) DIATECH INC
                                                                                                                                                                                                                                                         GHRPLDK 7
                                                                                                                                                                                                                                                                             GHRPLDK 7
                                                                                                                                                                                          Sequence 28 AA;
                                                                                                                                                                                                                                                                                                                                                                           01-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9533498-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
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                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                       ADD12888;
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tumours that express somatostatin receptors; leukocytes; atherosclerotic plaque, and deep vein thrombosis. Attachment of (II) to a sidechain avoids any interference with the specific binding properties of (I) and makes possible derivatisation of cyclic peptides (which are more resistent to proceolysis). Images may be recorded only a few minutes after injection of SIA. This is the amino acid sequence of a peptide associated with the imaging methods of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to peptides based on the alpha- and beta-chain sequences of fibrin/fibrinogen, which are capable of acting as fibrin antagonists. These are used for the therapy of local and generalised inflammation associated with infection, autoimmune reactions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptides or proteins based on fibrin or fibrinogen sequences, useful for combating fibrin-mediated disorders such as inflammation, transplant rejection, arteriosclerosis and reperfusion damage.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 100.0%; Score 41; DB 2; Length 28; Similarity 100.0%; Pred. No. 0.097; 7; Conservative 0; Mismatches 0; Indels
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Pred. No. 0.097;
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GHRPLDK 7
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 28 AA;
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New peptides are claimed which are leukocyte binding peptides having covalently bound to them a moiety which can bind a Tc-99m radiolabel. The epetides having Tc-99m bound to them are useful as scintigraphic imaging agents for imaging sites of infection and inflammation in the mammalian body, e.g. caused by ischaemia, inflammatory bowel disorder, arthritis or theores. The present sequence is a specifically claimed example of such a peptide derived from fibrinopeptide B chain. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                    Leukocyte binding peptide; fibrinopeptide B chain; scintigraphic imaging; inflammatiom site; technetium 99m.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scintigraphic imaging agent for sites of inflammation - comprising leukocyte-binding peptide bound technetium-99m via binding moiety.
                                                                                                   Leukocyte-binding peptide which can bind to technetium-99m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 41; DB 2; Length 30; ilarity 100.0%; Pred. No. 0.11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Targeting moiety, stabilisation; radiopharmaceutical; hydrophilic thioether; hydrophilic 6-hydroxy-chroman.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lister-James
                                                                                                                                                                                                                                                                                     "acetamidomethyl-Cys"
                                                                                                                                                                                                                                                      /note= "picolinoyl-Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Targeting moiety peptide SEQ ID NO:5.
                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP56240 standard; peptide; 30 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 15; Page 31; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Buttram S,
                                                                                                                                                                                                                                                                                                                                                                                       93WO-US002320
                                                                                                                                                                                                                                                                                                                                                                                                                      92US-00851074
                                                   (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1993-303154/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIAT-) DIATECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lees RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
hes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GHRPLDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 30 AA;
                                                                                                                                                                                                                       Key
Modified-site
                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                       12-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAR-1992;
                                                                                                                                                                                                                                                                                                                      W09317719-A1
                                                   25-MAR-2003
                                                                      05-AUG-1994
                                                                                                                                                                                                                                                                                                                                                      16-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-MAR-2003
                                                                                                                                                                                        Synthetic.
                    AAR42546;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dean RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP56240;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New peptides are claimed which are leukocyte binding peptides having , covalently bound to them a moiety which can bind a Tc-99m radiolabel. The peptides having Tc-99m bound to them are useful as scintigraphic imaging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      agents for imaging sites of infection and inflammation in the mammalian body; eg. caused by ischlamia, inflammatory bowel disorder, arthritis or tumours. The present sequence is a specifically claimed example of such a peptide derived from fibrinopeptide B chain. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                   Leukocyte binding peptide; fibrinopeptide B chain; scintigraphic imaging;
inflammatiom site; technetium 99m.
                                                                                                                                                                                                                                                                                                                                                                                                                   /label= OTHER
/note= "BAT, i.e. N6,N9-bis(2-methyl- 2-mercaptopropyl)-
6,9-diazanonanoic acid"
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scintigraphic imaging agent for sites of inflammation - comprising leukocyte-binding peptide bound technetium-99m via binding moiety.
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                                                                                                                                                                                                                                                                    Leukocyte-binding peptide which can bind to technetium-99m.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 41; DB 2; Length 29; 100.0%; Pred. No. 0.1;
   .0; Indels
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 Mismatches
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AAR42546
ID AAR42546 standard; peptide; 30 AA.
                                                                                                                                                  AAR42547 standard; peptide; 29 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Arg-NH2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dean RT, Lees RS, Buttram S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93WO-US002320.
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                                                                                                                                                                                                                   (revised)
(first entry)
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1993-303154/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DIAT-) DIATECH INC.
                                  GHRPLDK 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       correct PN field.)
                                                     GHRPLDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 29 AA;
                                                                                                                                                                                                                                                                                                                                                                                    Key
Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-MAR-1993;
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                                                                                                                                                                                                                  25-MAR-2003
05-AUG-1994
7;
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                                                                                                                                                                                                                                                                                                                                                     Synthetic
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Best Local
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AAR42547
AAR42647
AAR

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Gaps

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Matches

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1 GHRPLDK
                 US2003072709-A1
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                                                                                                                                                                                                                                                                                                                                                                          Sequence 30 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2003103895-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                     compositions.
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                                        17-APR-2003
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                                                                                                                                                      Cyr JB,
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                     (CYRJ/)
                                                                                                                                (PEAR/)
                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                             The present invention describes a composition (C) comprising a radiopharmaceutical precursor and a stabiliser selected from hydrophilic thioether (I) and/or hydrophilic 6-hydroxy-chroman derivative (II). Also described: (1) stabilishing a radiopharmaceutical comprising: combining the radiopharmaceutical precursor with (I) and/or (II) in a container, and adding a radionuclide to the container; and (2) a kit comprising a sealed vial containing the radiopharmaceutical precursor; and il) and/or (II). (C) can be used to increase the shelf life of diagnostic and therapeutic radiopharmaceutical precursors in nuclear medicine. The stabilisers maintain the radiocharmaceutical purity of the radiopharmaceutical containing the radiocharmaceutical precursors in nuclear medicine. The stabilisers maintain the radiocharmaceutical precursors in containing a vide variety of radiopharmaceutical. (C) is suitable for stabilising a wide variety of radiopharmaceuticals. The present sequence represents a specifically contained targeting moiety peptide for a composition from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                 Composition useful for increasing shelf life of diagnostic and therapeutic radiopharmaceuticals, comprising radiopharmaceutical precursor and hydrophilic thioether and/or hydrophilic 6-hydroxy-chroman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Radiopharmaceutical composition stabilising hydrophilic thioether #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            radiopharmaceutical precursor; hydrophilic thioether;
radiopharmaceutical composition; diagnosis; therapy; shelf life;
diagnostic radiopharmaceutical; therapeutic radiopharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 41; DB 6; Length 30; 100.0%; Pred. No. 0.11; ive 0; Mismatches 0; Indels
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/note= "C-terminal amide"
Location/Qualifiers 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADE64331 standard; peptide; 30 AA.
                          /note= "amidated
                                                                                                                                                                                                                                                                                            Claim 15; Page 48; 64pp; English
                                                                                                                  24-OCT-2000; 2000US-00694992.
24-OCT-2000; 2000US-00695360.
24-OCT-2000; 2000US-00695494.
                                                                                             24-OCT-2001; 2001WO-US050423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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Best Local Similarity 100.
                                                                                                                                                                                       Pearson DA;
                                                                                                                                                                (DIAT-) DIATIDE INC.
                                                                                                                                                                                                            WPI; 2003-092782/08.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 30 AA;
                                               WO200260491-A2
     Key
Modified-site
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Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JAN-2004
                                                                       08-AUG-2002
                                                                                                                                                                                                                                                                     derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
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                                                                                                                                                                                       Cyr JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 25
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Composition used in diagnosis and therapy comprises stabilizing amount of hydrophilic thioether and radiopharmaceutical precursor or peptide or benzodiazepine derivative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention decribes a composition comprising a radiopharmaceutical precursor and a stabilising amount of a hydrophilic thioether. The composition is useful as stabiliser of radiopharmaceutical compositions for use in diagnosis and therapy. The composition is particularly useful for increasing the shelf life of diagnostic or therapeutic radiopharmaceuticals. This the amino acid sequence of a hydrophilic thioether used in the method of stabilising radiopharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  radiopharmaceutical precursor; hydrophilic 6-hydroxy-chroman derivative; stabiliser; radiopharmaceutical composition; diagnosis; therapy; shelf life.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 13; SEQ ID NO 5; 19pp; English.
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29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADH58575 standard; peptide; 30 AA.
24-APR-2002; 2002US-00131543.
                                                            24-OCT-2000; 2000US-00694992.
24-OCT-2001; 2001WO-US050423.
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24-OCT-2001; 2001WO-US050423.
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                                                                                                                                                                                                                                                                 Pearson DA;
                                                                                                                                                           CYR J E.
PEARSON D A.
                                                                                                                                                                                                                                                                                                                           WPI; 2004-040976/04.
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AAG00151
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                                                                                                                                                              The invention describes a composition comprising a radiopharmaceutical precursor and a hydrophilic 6-hydroxy-chroman derivative. The composition is useful as stabilisers of radiopharmaceutical compositions for use in diagnosis and therapy. The composition is particularly useful for increasing the shelf life of diagnostic or therapeutic radiopharmaceuticals. This is the amino acid sequence of a peptide used in the stabilisation of radiopharmaceutical compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cytokine; cell proliferation; cell differentiation; growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bone disorder; osteoporosis; vascular growth disorder;
tissue regeneration; wound healing; infection; immune disorder;
cell culture; dung screening; gene therapy; antiinflammatory;
antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
                                                                        Compositions, useful as stabilizers, or for increasing shelf life, of radiopharmaceuticals for use in diagnosis or therapy, comprises radiopharmaceutical precursor, hydrophilic thioether and hydrophilic 6-hydroxy-chroman derivative.
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia;
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                                                                                                                                                                                                                                                                                           100.0%; Score 41; DB 8; Length 30; 100.0%; Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human beta-fibrinogen homologue, SEQ ID NO:1709.
                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                      Claim 16; SEQ ID NO 5; 17pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB11339 standard; peptide; 87 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antifungal; vulnerary; antiulcer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-FEB-2001; 2001WO-US003800
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27-APR-2000; 2000US-00560875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                  7; Conservative
(PEAR/) PEARSON D A.
                         Pearson DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-457740/49.
N-PSDB; ABA08583.
                                                  WPI; 2004-106449/11
                                                                                                                                                                                                                                                                                                                                                                    CHRPLDK 10
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                           1 GHRPLDK 7
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                                                                                                                                                                                                                                                                  Sequence 30 AA;
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                         Cyr JE,
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condition also relates to vectors and recombinant borspectures. Sequences ABA08225-ABA0924 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, and methods of identifying compounds which to polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth activity; in memomodulatory activity; tissue growth activity; chrombolycic or chemokinetic activities; paemostatic or may be conditions activities, receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis.

Compositions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoleted disporders (e.g., myeloid or lymphoid cell cancers, haematopoletic disporders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arreadis activities may be used to promote wound repair (or nucleic acids encoding them) may be used to promote wound repair (or nucleic acids encoding them) may be used to promote wound tell souterial and fungal infections in addition to immune disorders.

Dependent of growth. For example, such polypeptides may be used to commune to viral, near the angular or arthrity may be used in cell cultures to gromote cell growth. For example, such polypeptides may be used to neuroepithelalial cells cancer activity may be used by any any and any 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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nan proteins and DNA encoding sequences useful for preventing, treating ameliorating a medical condition in a mammalian subject e.g. arthritis
                                                                                                                                                                                                                         Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                      Claim 20; Page 167; 1963pp; English.
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Best Local Similarity
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       Human proteins
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                                                                       and cancer.
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colypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying at therapeutic agent corpus in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptides. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins or are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopolesis; and in bone, cartilage, tendon and an autimulation; as anti-inflammatory agents; and in treatment of leukaemias. ANU29510-ANU33304 represent the amino acid sequences of novel human secreted proteins of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                               Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                                                                                                      The invention relates to novel human secreted polypeptides. The
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                                                                                                                      Claim 20; Page 752; 765pp; English.
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18-MAY-2000; 2000US-00577409
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WPI; 2001-611725/70
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 140 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is a polypeptide encoded by one of a large number of 5' ESTS derived from mRNAs encoding secreted proteins. The 5' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
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stem cell proliferation, haematopoiesis, nerve tissue regeneration,
immune suppression, immune stimulation, anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                        diagnostic, forensic, gene therapy and chromosome mapping procedures.
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                                                                                                                                                                                                                                                                                                                                                                                                       Claim 13; SEQ ID NO 4232; 71pp + Sequence Listing; English.
                                                                                                                                                                                         Giordano J;
                                                                                                                                                                                            Duclert A,
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                                            21-FEB-2000; 2000EP-00200610.
                                                                                           99US-0122487P
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26-JAN-2001; 2001US-00770160
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1es 7; Conservative
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                                                                                                                                                                                                                                         WPI; 2000-500381/45
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                                                                                                                                                                                                                                                               N-PSDB; AAC00157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 118 AA;
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                                                                                                                                          GEST ) GENSET
                                                                                         26-FEB-1999;
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The invention relates to human polynucleotides (AAI79941-AAI93841) and cytokine, cells (AAO0010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     obtaining cDNAs and genomic DNAs that correspond to 3 mais and diagnostic, forensic, gene therapy and chromosome mapping procedures.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secreted protein, SEQ ID NO: 4231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG00150 standard; protein; 150 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-FEB-2000; 2000EP-00200610
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                               41 GHRPLDK 47
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                                                                                                                                                                                                                                                    Sequence 141 AA;
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The present sequence is a polypeptide encoded by one of a large number of 5' ESTS derived from mRNAs encoding secreted proteins. The 5' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated primed cDNA libraries. Such ESTS are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where included. 5' ESTS are derived from mina, with intext 5' ends and can included. 5' ESTS are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTS are also used in diagnostic, forensic, gene therapy and chromosome

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mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                   Human; cytokine; cell proliferation; cell differentiation; gene therapy; accine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
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J, Zhang J, Ren F, Chen R, Wang ZW;
Goodrich R;
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                                                                               Score 41; DB 3; Length 150;
Pred. No. 0.7;
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                                                                                                                                                                                                                                                          AAM78493 standard; protein; 453 AA.
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Wang D, Wang J
, Wejhrman T, G
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100.0%;
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2000US-00560875.
2000US-00598075.
2000US-00620325.
2000US-00654936.
                                                                                                                                                                                                                                                                                                                                                       Human protein SEQ ID NO 1155.
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2000US-00693325.
2000US-00728422.
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                                                                                                              7; Conservative
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GHRPLDK 51
                                                                             Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                            1 GHRPLDK 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang YT, Liu C,
Ma Y, Zhao QA, V
Xue AJ, Yang Y,
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                                                 Sequence 150 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-APR-2000;
20-JUN-2000;
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20-OCT-2000;
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Gaps

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Score 41; DB 8; Length 455. Pred. No. 2.6;

100.0%;

Sequence 455 AA;

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us-09-424-940a-1.rag

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The invention relates to novel diagnostic and therapeutic polymucleotides selected from one of the 2722 sequences defined in the specification. A control of the invention may have a use in gene therapy. The human diagnostic and therapeutic polymucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine cutoimmune/inflammatory disorder, developmental disorders, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp confluence may also be used in genetic mapping, in identifying individuals confluence may also be used in genetic mapping, in identifying individuals confluence pological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline confluence. The present sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
                                                                                                                                                                                                ABM85149 standard; protein; 455 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 27; Page; 190pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                              12-SEP-2003; 2003WO-US028227.
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                                                                                                                                                                                                                                                          (first entry)
                                       Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INCY-) INCYTE CORP.
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                                                                                                         1 GHRPLDK 7
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Sequence 453 AA;
                                                                                                                                                                                                                                                                                                                                                                                  WO2004023973-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene mapping
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                             Query Match
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gene therapy; human diagnostic and therapeutic polynucleotide; dithp
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Query Match
Best Local Similarity 100.
Matches 7; Conservative
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Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietze
Patury S,, Shi X, Suarez CJ;
                                                                                                          Gaps
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                                     100.0%; Score 41; DB 4; Length 453; 100.0%; Pred. No. 2.6;
                                                                                                      0; Indels
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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnost a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp concerns also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single mucleotide polymorphisms, as molecular weight markers, and for somatic or germline polymorphisms, as molecular weight markers, and for somatic or germline invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                              Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen I
Patury S, Shi X, Suarez CJ;
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12-SEP-2002; 2002US-0410260P.
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N-PSDB; ACN43802.
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Query Match

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The invention relates to novel diagnostic and therapeutic polymucleotides selected from one of the 2722 sequences defined in the specification. A polymucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polymucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, dastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp concluse may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline polymorphisms, as molecular weight markers, and for somatic or germline invention. Note: The sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wn MC, Stuve LL;
Lagace RE, Spiro PA, Stewart RA, Wingrove J, Vitt UA, Kirton SS;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
Patury S, Shi X, Suarez CJ;
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                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                             gene therapy; human diagnostic and therapeutic polynucleotide; dithp
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    8; Length 455;
                                           0; Indels
                                                                                                                                                                                                                                                                                                                                        Human diagnostic and therapeutic pprotein SEQ ID NO:5401.
    Score 41; DB 8
Pred. No. 2.6;
                                           Mismatches
                                                                                                                                                                                                                   ABM85152 standard; protein; 474 AA.
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  100.08;
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12-SEP-2002; 2002US-0410260P.
                                                                                                                                                                                                                                                                                                 (first entry)
Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                     GHRPLDK 51
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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp concluse may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single mucleotide polymorphisms, as molecular weight markers, and for somatic or germline polymorphisms, as molecular weight markers a dithp protein of the invention. Note: The sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
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Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Blder LV;
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen BJ, Wu MC, Stuve LL;
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kircon ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
Patury S, Shi X, Suarez CJ;
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                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
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Similarity 100.0%; Score 41; DB 8; Length 474;
7; Conservative 0; Mismatches ο τηλη
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                                                                                                                                                                                                                                               ABM84478 standard; protein; 474 AA.
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12-SEP-2002; 2002US-0410260P.
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                            Best Local Similarity
Matches 7; Conserv
                                                                                               1 GHRPLDK 7
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DB 8;

Score 41;

100.08;

Query Match

Sequence 474 AA;

Gaps

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The invention relates to novel diagnostic and therapeutic polymucleotides selected from one of the 2722 sequences defined in the specification. A polymucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polymucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine disorder, neurological disorder, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline polymorphisms, are molecular weight markers and for somatic or germline invention. Note: The sequence fact for this patent is not represented in the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   wright RJ, Bruns CM, Marjanovic MM, Shen F; e TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV; Delegeane AM, Panesar IS, Banville SC, Reddy TP; Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH; Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL; Spiro PA, Stewart RA, Wingrove J, Vitt UA, Kirton ES; GM, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen Shi X, Suarez CJ;
                                                                                                                                                                                                                                                                                                                       gene therapy; human diagnostic and therapeutic polynucleotide; dithp
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                           0; Indels
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       Pred. No. 2.7;
100.0%; Prec. ....
                                                                                                                                                                                 ABM84481 standard; protein; 474 AA.
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       Best Local Similarity 100.
Matches 7; Conservative
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                                                                                            GHRPLDK 51
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S, Shi X,
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Peralta CH,
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Gietzen D;

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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 272 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnost a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine autoimmune/inflammatory disorder, developmental disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp concernisms may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline polymorphisms, as molecular weight markers, and for somatic or germline invention. Note: The sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
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   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shen F;
SJ, Elder LV;
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   Indels
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 Mismatches
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12-SEP-2002; 2002US-0410260P
7; Conservative
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                                                                          51
                                     1 GHRPLDK 7
                                                                        45 GHRPLDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ACN43134
                                                                                                                                                                                                                                                                                                                                                                                              WO2004023973-A2.
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                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                              18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2004
                                                                                                                                                                                                          ABM84482;
Matches
                                                                                                                                RESULT 38
                                                                                                                                                    ABM84482
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Gaps

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100.0%; Score 41; DB 8; Length 474; llarity 100.0%; Pred. No. 2.7; Conservative 0; Mismatches 0; Indels

Best Local Similarity Matches 7; Conserv

Score 41; DB 8; Length 474; Pred. No. 2.7;

100.0%;

Query Match Best Local Similarity

Query Match

GHRPLDK

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Human diagnostic and therapeutic pprotein SEQ ID NO:5400.
                            ABM85151 standard; protein; 474 AA.
                                                                                                                                                                                                                                                       Claim 27; Page; 190pp; English.
                                                                                                                   12-SEP-2003; 2003WO-US028227
                                                                                                                              12-SEP-2002; 2002US-0410259P
12-SEP-2002; 2002US-0410260P
                                                  18-NOV-2004 (first entry)
                                                                                                                                               (INCY-) INCYTE CORP.
                                                                                                                                                                                                           WPI; 2004-329368/30.
GHRPLDK 51
                                                                                                                                                                                          Kwong M, P
S. Shi X,
                                                                                                                                                                                                                 N-PSDB; ACN43803
                                                                                             WO2004023973-A2.
                                                                                                                                                                                                                                                                                                                                                              Sequence 474 AA;
                                                                                  Homo sapiens
                                                                                                                                                                Harthshorne
                                                                                                                                                                          Stevens KA,
Peralta CH,
                                                                                                                                                          Schmidt JP,
                                                                                                         25-MAR-2004
                                                                                                                                                                                                Patury S,
                                                                                                                                                                      Mooney EM,
                                                                                                                                                                                     Lagace RE,
45
                                       ABM85151;
                  RESULT 39
                      ABM8515
                            셤
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The invention relates to a composition comprising several cDNAs that are differentially expressed in a liver disorder. The composition is useful for treating liver disorder such as hyperlipidaemia, hypertension, type II diabetes, tumours of the liver and disorders of the inflammatory and immune response. The composition is useful for a high-throughput method of several molecules or compounds to identify a ligand which specifically binds a cDNA. A protein encoded by the cDNA is useful for high-throughput method for using a protein to screen several molecules or compounds to identify at least one ligand which specifically binds the protein which involves combining the protein encoded by the cDNA with several of molecules or compounds under conditions to allow specific or binding, and detecting specific binding between the protein and a molecule or compound, therefore identifying a ligand which specifically chinds the protein. The composition is useful for detecting and quantifying differential gene expression, can be used in gene therapy, to formulate prognosis and to design a treatment regimen and to monitor the efficacy of treatment. The present sequence represents the amino acid sequence of a protein encoded by a cDNA differentially expressed in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Composition comprising several cDNAs that are differentially expressed in treated human C3A liver cell cultures, useful for treating liver
                                                                                                                                                                                                                                                                                                                                                                                                                       human; liver disorder; hyperlipidaemia; hypertension; type II diabetes; tumour; liver; inflammatory disorder; immune response disorder; high-throughput screening; differential gene expression; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Length 488;
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                                                                                                                                                                                                                                                                                                                                                                    Human protein expressed in a liver disorder #11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 41; DB 8
100.0%; Pred. No. 2.8;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 33; 41pp; English.
                                                                                                                                                                                                 ADE76868 standard; protein; 488 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUL-2001; 2001US-00919039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUL-2000; 2000US-0222113P.
                                                                                                                                                                                                                                                                                                               29-JAN-2004 (first entry)
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Best Local Similarity 100.
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                                   |||||||
45 GHRPLDK 51
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1 GHRPLDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-JUN-2003.
                                                                                                                                                                                                                                                      ADE76868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaser MR;
                                                                                                                                        RESULT 40
                                                                                                                                                                      ADE76868
                                                                                                                                                                                                                                                      The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A puricleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine caused to diagnosial disorder, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp conflections manner and also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp protein of the gene therapy. The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wright RJ, Bruns CM, Marjanovic MM, Shen F;
TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Blanchard UL, Panzer SR, Wang X, Au AP, Gerstin EH;
Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
GM, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
Shi X, Suarez CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
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Gaps

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100.0%; Score 41; DB 8; Length 474; 100.0%; Pred. No. 2.7; cive 0; Mismatches 0; Indels

Local Similarity 100.

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Query Match

1 GHRPLDK 42 GHRPLDK

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Query Match
Best Local Similarity
Matches 7; Conserv
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6, Appli
4, Appli
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5, Appli
1709, Ap
33, Appl
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                                                                                                                                                                                                                                                 (without alignments)
27.728 Million cell updates/sec
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                                                                                                                                                                                                                   June 1, 2005, 11:44:05 ; Search time 87.2667 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | Cgn2_6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US06 PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-459-030B-294
US-10-131-543-5
US-10-131-546-5
US-10-131-346-5
US-10-1415-024-5
US-10-276-774-1709
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US-10-142-935-9
US-10-142-935-8
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US-10-142-935-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GHRPLDK 7
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Perfect score:
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                                                                                                                                                                                                               Run on:
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        14
        36
        87.8
        16
        18
        US-10-378-674-7
        Sequence 7, Appliance 15

        15
        36
        87.8
        479
        14
        US-10-142-955-5
        Sequence 17.165.

        16
        87.8
        47.9
        14
        US-10-1437-965-12627
        Sequence 12627, A

        18
        36
        87.8
        732
        14
        US-10-156-761-12627
        Sequence 12627, A

        20
        35
        85.4
        240
        14
        US-10-1437-963-182675
        Sequence 12627, A

        21
        35
        85.4
        240
        14
        US-10-17-161-1358
        Sequence 175814, Appliance 1826, Appli
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ALIGNMEN

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"US-10-450-073-6

"Sequence 6, Application US/10450073

"Bublication No. US20040132969A1

"GENERAL INFORMATION:

"APPLICANT: Melvin, William T

"APPLICANT: Thompson, William D

"APPLICANT: Thompson, William D

"APPLICANT: Antibodies, Peptides, Analogs and Uses Thereof

"TILE REFERENCE: 0380-093213USO

"CURRENT PILING DATE: 2001-12-12

"PRIOR FILING DATE: 2000-12-12

"PRIOR FILING
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TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY
TITLE OF INVENTION: CHROMANS
FILE REPERBUCE: 09744-018001
CURRENT APPLICATION NUMBER: US/10/131,546
CURRENT FILING DATE: 2002-04-24
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: Z000-10-24
PRIOR FILING DATE: Z000-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cyr, John E.
APPLICANT: Cyr, John E.
APPLICANT: Pearson, Daniel A.
TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: USUG HYDROPHILIC THIOETHERS
TITLE OF INVENTION: 09744-01601
CURRENT PAPLICATION NUMBER: US/10/131,543
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: PCT/US01/50423
PRIOR APPLICATION NUMBER: PCT/US01/50423
PRIOR APPLICATION NUMBER: PCT/US01/50423
PRIOR FILING DATE: 2001-10-24
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 30
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100.0%; Score 41; DB
Best Local Similarity 100.0%; Pred. No. 0.6
Matches 7; Conservative 0; Mismatches
    NUMBER OF SEQ ID NOS: 296
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 294
LENGTH: 28
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Publication No. US20030072709A1
GENERAL INFORMATION:
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Publication No. US20030103895A1
GENERAL INFORMATION:
APPLICANT: Cyr, John E.
APPLICANT: Pearson, Daniel A.
                                                                                                                                                         OTHER INFORMATION: peptide Bbeta
                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.(
Matches 7; Conservative
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; LOCATION: 30
US-10-131-543-5
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US-10-131-543-5
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         Sequence 6, Application US/10142935
Publication No. US20030044418A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HOOK, Magnus A.O.
TITLE OF INVERTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATI
FILE REFERENCE: P07201UG18, BAS
CURRENT APPLICATION NUMBER: US/10/142, 935
CURRENT PILING DATE: 2002-05-13
PRIOR PHILNG DATE: 2001-05-13
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 6
LENGTH: 20
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Publication No. US20030044418A1
GENERAL INFORMATION:
APPLICANT: DAVIS, Stacey
APPLICANT: HOOK, Magnus A.O.
TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATI
FILE REFERENCE: P07201US01/BAS
CURRENT APPLICATION NUMBER: US/10/142,935
CURRENT FILING DATE: 2002-05-13
PRIOR FILING DATE: 2001-05-13
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
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Publication No. US20040192596A1
GENERAL INFORMATION:
APPLICANT: Petzelbauer, Peter
TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
FILE REFERENCE: A35859 PCT US/10/459,030B
CURRENT APPLICATION NUMBER: 2003-06-11
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hag 0; Indels
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PRIOR FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: AT 2063/2000
PRIOR FILING DATE: 2000-12-12
                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-142-935-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-142-935-4
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Best Local Similarity 100.
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Best Local Similarity 100.
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US-10-142-935-6
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LENGTH: 25
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Sequence 1709, Application US/10276774

Publication No. US20040053245A1

GENERAL INPORMATION:

APPLICANT: Hyesq, Inc.

APPLICANT: Tang, Y, Tom et al

TITLE OF INVENTION: US20040053245A1e1 Nucleic Acids and Polypeptides

FILE REFERENCE: 21272-030

CURRENT APPLICATION NUMBER: US/10/276,774

CURRENT APPLICATION NUMBER: 09/560,875

PRIOR FILING DATE: 2000-04-27

PRIOR FILING DATE: 2000-04-27

SOFTWARE: CLUSTON NUMBER: 09/496,914

PRIOR FILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 2700

SEQ ID NO 1709

LENGTH: 87
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Publication No. US20030108871A1
GENERAL INFORMATION:
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
TILE REPERBURE: PA-0035 US
CURRENT RAPPLICATION UNDMER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
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100.0%; Score 41; DB 15; Length 87;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 7; Conservative 0; Mismatches 0: Thiale
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OTHER INFORMATION: Xaa = any amino acid or nothing
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                    PRIOR APPLICATION NUMBER: US 09/695,360
PRIOR FILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PARKSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 30
                                                                                                                                                                                                                                                                 OTHER INFORMATION: Synthetic construct
                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence
    PRIOR FILING DATE: 2000-10-24
                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
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ORGANISM: Homo sapiens
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; LOCATION: 30
US-10-415-024-5
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US-10-276-774-1709
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TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY
TITLE OF INVENTION: GRECOMANS
FILE REPERBENCE: 09744-015W01
CURRENT APPLICATION NUMBER: US/10/415,024
FRIOR APPLICATION NUMBER: US 09/694,992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/10131346
PUblication No. US20030103899A1
GENERAL INFORMATION:
APPLICATION NO. US20030103899A1
GENERAL INFORMATION:
TITLE OF INVENTION: USTED HYPOPHILIC 6-HYDROXY CHROMANS
TITLE OF INVENTION: USTED US/10/131,346
CURRENT APPLICATION NUMBER: US/10/131,346
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2001-10-24
PRIOR PLILING DATE: 2001-10-24
PRIOR FILING DATE: 2001-10-24
PRIOR PRILING DATE: 2001-10-24
SOFTWARE: FRAELSEQ for Windows Version 4.0
SEQ ID NO 5
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100.0%; Pred. No. 0.7
tive 0; Mismatches
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PRIOR FILING DATE: 2001-10-24
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                               OTHER INFORMATION: Synthetic construct PRATURE:
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OTHER INFORMATION: Synthetic construct
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                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
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Best Local Similarity 100.
Matches 7; Conservative
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; LOCATION: 30
US-10-131-546-5
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; LOCATION: 30
US-10-131-346-5
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US-10-131-346-5
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                                                               SEQ ID NO 5
LENGTH: 30
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Sequence 8, Application US/10142935
Publication No. US2003004418A1
EMERRAL INFORMATION:
APPLICANT: DAVIS, Stacey
APPLICANT: DAVIS, Stacey
APPLICANT: DAVIS, Stacey
TITLE OF INVENTION:
METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATIC,
FILE REFERENCE: P07201US01/BAS
CURRENT APPLICATION NUMBER: US/10/142,935
CURRENT FILING DATE: 2002-05-13
PRIOR PELING PATE: 2001-05-13
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 8
LENGTH: 15
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; Sequence 7, Application No. US/20040006209A1

; Dublication No. US/20040006209A1

; Publication No. US/20040006209A1

; Publication No. US/20040006209A1

; APPLICANT: PATTI, Joseph M.

; APPLICANT: PATTI, Joseph M.

; TITLE OF INVENTION: MONOCLONDL AND POLYCLONAL ANTIBODIES RECOGNIZING COAGULASE-NEGATIVITION: MONOCLONDL STAPPLICANTON NUMBER: US/10/378,674

; CURRENT APPLICATION NUMBER: US/10/378,674

; CURRENT PILING DATE: 2002-03-05

PRIOR FILING DATE: 2002-03-05

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PatentIn version 3.1

SEQ ID NO 7

LENGTH: 16
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                                Score 36; DB 14; Length 10; Pred. No. 2.3;
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Pred. No.
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US-10-142-935-5
; Sequence 5, Application US/10142935
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          Query Match
Best Local Similarity 100.
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 6; Conservative
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Sequence 9, Application US/10142935

Publication No. US20030044418A1

Sequence 9, Application US/00044418A1

Publication No. US20030044418A1

APPLICANT: DAVIS, Stacey

APPLICANT: HOOK, Magnus A.O.

TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATI
FILE REFRENCE: P07201US01/BAS

CURRENT FILING DATE: 2002-05-13

PRIOR APPLICATION NUMBER: US 60/290,072

PRIOR FILING DATE: 2001-05-13

NUMBER OF SEQ ID NOS: 11

SEQ ID NOS: 11

SEQ ID NO 9

LENGTH: 10
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TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
CURRENT APPLICATION NUMBER: US/10/017,724

PRIOR APPLICATION NUMBER: US 60/317,178

PRIOR APPLICATION NUMBER: US 60/317,178

PRIOR FILING DATE: 2001-09-05

PRIOR FILING DATE: 2001-10-16

NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 491;
                                                                                                                                                                                                                                                                                  100.0%; Score 41; DB 10; Length 488; 100.0%; Pred. No. 11;
                                                                                                                                                                                          ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 3393861CD1
US-09-919-039-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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100.0%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL Program
SEQ ID NO 33
LENGTH: 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 6, Application US/10017724; Publication No. US20030099958A1; GENERAL INFORMATION:
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Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo Sapiens
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Can Yongwei
APPLICANT: Can Yongwei
APPLICANT: Can Yongwei
APPLICANT: Can Yongwei
APPLICANT: Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
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100.0%; Pred. No. 1.6e+02;
ive 0; Mismatches 0; Indels
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US-10-437-963-182675
                       APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLECTIDES
FILE REPERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 12627
LENGTH: 732
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                                                                                                                                                                                                                                                                          , ORGANISM: Streptomyces avermitilis US-10-156-761-12627
         SAKAKI, YOSHIYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.'
Matches 6, Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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94 GHRPLD 99
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Publication No. US2003004418A1
GENERAL INFORMATION:
APPLICANT: DAVIS, Stacey
APPLICANT: DAVIS, Stacey
APPLICANT: HOOK, Magnus A.O.
TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATI
FILE REPRENCE: PO7201US01/BA2
CURRENT APPLICATION NUMBER: US/10/142,935
CURRENT APPLICATION NUMBER: US 60/290,072
PRIOR APPLICATION NUMBER: US 60/290,072
PRIOR PLING DATE: 2001-05-13
NUMBER OF SEQ ID NOS: 11
SQC ID NOS: 12
SQC ID NOS: 12
SQC ID NOS: 12
SQC ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: File Molecules and Other Molecules Associated With TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement; PILE REFERENCE: 38-21(53221)B; CURRENT APPLICATION NUMBER: US/10/437,963; CURRENT PILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 127165 LENGTH: 479
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100.0%; Pred. No. 1e+02;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No.
0; Mismatches
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GENERAL INFORMATION: APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUNN: APPLICANT: HORIXAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 127165, Application US/10437963; Publication No. US20040123343A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-142-935-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Bucharov, Andrey A.
APPLICANT: Barbazuk, Brad
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Matches 6; Conservative
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ORGANISM: Oryza sativa
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US-10-156-761-12627
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PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
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Publication No. US20030143668A1
GENERAL INFORMATION:
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Publication No. US20030198955A1
GENERAL INFORMATION:
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Ballinger, Robert
Kekuda, Ramesh
      2002-12-18
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Gerlach, Valerie
Sciore, Paul
Smithson, Glennda
Peyman, John
MacDougall, John
Stone, David
Vernet, Corine
Shenoy, Suresh
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Spytek, Kimberly
Casman, Stacie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
                                                            NUMBER OF SEQ ID NOS: 2430
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 450
LENGTH: 305
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
US-10-017-161-468
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      CURRENT FILING DATE:
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100.0%; Pred. No. 83;
ive 0; Mismatches 0; Indels
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US-10-017-161-1358

$ Sequence 1358, Application US/10017161

$ Publication NO. US20030143668A1

$ GENERAL INFORMATION:

$ APPLICANT: SUWA, MAKIKO

$ APPLICANT: AKIYAMA, YUTAKA

$ APPLICANT: AKIYAMA, YUTAKA

$ APPLICANT: ARUTANNI, HIROYUKI

$ TILLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS

$ FILE REFERENCE: 084335/0152

$ CURRENT APPLICATION NUMBER: US/10/017,161

$ CURRENT PILING DATE: 2002-12-18

$ PRIOR PILING DATE: 2001-06-18

$ PRIOR FILING DATE: 2001-06-18

$ NUMBER OF SEQ ID NOS: 2430

$ SOFTWARE: Patentin Ver: 2.1

$ SEQ ID NO 1358
                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT3847_129779C.1.pep
US-10-424-599-175814
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Publication No. US20030143668A1
GENERAL INFORMATION:
APPLICANT: SUWA, MAKIKO
APPLICANT: SUWA, KIYOSHI
APPLICANT: ASI, KIYOSHI
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REPERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
                                                                                                                                                                                      LOCATION: (1)..(74)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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COCATION: (8)...(41)
COTHER INFORMATION: Variable amino acid
US-10-017-161-1358
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 6; Conservative
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ORGANISM: Homo sapiens
                                                                                                                       TYPE: PRT
ORGANISM: Glycine max
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                                                                               SEQ ID NO 175814
LENGTH: 74
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US-10-017-161-450
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                                                       Score 35; DB 14; Length 305;
Pred. No. 1e+02;
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85.4%; Score __.
100.0%; Pred. No. 1e+0.
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PRIOR APPLICATION NUMBER: JP 2001-246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 404
LENGTH: 305
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Best Local Similarity 100.
Matches 6; Conservative
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CORGANISM: Homo sapiens
US-10-292-798-418
                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-798-404
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Publication No. US20030235833A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: AASAL, KIYOSHI
APPLICANT: ARIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
CURRENT APPLICATION NUMBER: 10/017,161
PRIOR PILING DATE: 2002-11-13
PRIOR FILING DATE: 2001-12-18
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TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
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CURRENT APPLICATION NUMBER: US/10/025,806
CURRENT FILING DATE: 2001-12-19
FRIOR APPLICATION NUMBER: 60/256,635
FRIOR PILING DATE: 2001-12-18
FRIOR PILING DATE: 2001-10-18
FRIOR PILING DATE: 2001-01-04
FRIOR FILING DATE: 2001-06-19
FRIOR PILING DATE: 2001-06-19
FRIOR APPLICATION NUMBER: 60/299,327
FRIOR PILING DATE: 2001-01-24
FRIOR PILING DATE: 2001-01-24
FRIOR FILING DATE: 2001-01-24
FRIOR FILING DATE: 2001-02-08
FRIOR FILING DATE: 2001-02-28
FRIOR FILING DATE: 2001-02-28
FRIOR FILING DATE: 2001-02-22
FRIOR FILING DATE: 2001-02-22
FRIOR APPLICATION NUMBER: 60/275,946
FRIOR FILING DATE: 2001-03-14
FRIOR FILING DATE: 2001-04-23
FRIOR FILING DATE: 2001-04-23
FRIOR FILING DATE: 2001-04-23
FRIOR FILING DATE: 2000-02-16
FRIOR FILING DATE: 2001-04-18
FRIOR FILING DATE: 2000-02-16
FRIOR FILING DATE: 2000-01-04
FRIOR FILING DATE: 2001-04
FRIOR FILING DA
                                                                    Tchernev, Velizar
Anderson, David
Gusev, Vladimir
Malyankar, Uriel
                                                                                                                                                                 Malyankar, Uriel
Zhong, Haihong
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Best Local Similarity 100.
Matches 6; Conservative
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ORGANISM: Homo sapiens
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220 HRPLDK 225
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US-10-292-798-404
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LENGTH: 305
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Sequence 2, Application US/10041615

Publication No. US20040014038A1

GENERAL INFORMATION:

APPLICANT: Edinger, Shlomit R

APPLICANT: Rekuda, Ramesh

APPLICANT: Muralidhara

APPLICANT: Muralidhara

APPLICANT: Validigaru, Muralidhara

APPLICANT: Validigaru, Muralidhara

APPLICANT: Validigaru, Muralidhara

TITLE OF INVENTION: NO. US20040014038A1e1 GPCR-Like Proteins and Nucleic Acids Encodir

CURRENT PILING DATE: 2001-01-03

PRIOR APPLICATION NUMBER: 60/259,552

PRIOR APPLICATION NUMBER: 60/250,544

PRIOR PILING DATE: 2001-01-09

PRIOR PILING DATE: 2001-01-09

PRIOR APPLICATION NUMBER: 60/277,405
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Sequence 418, Application US/10292798

Sequence 418, Application World 1 220030235833A1

GENERAL INFORMATION:

APPLICANT: SASI, KIYOSHI

APPLICANT: ABAINA, YUTAKA,

APPLICANT: ABURATANI, HIROYUKI

TILLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS

FILE REFERENCE: 084335/166

CURRENT FILING DATE: 2002-11-13

FRIOR APPLICATION NUMBER: 10/017,161

PRIOR FILING DATE: 2001-06-18

NUMBER OF SEQ ID NOS: 2070

SEQ ID NOS: 2070

SEQ ID NO 418

LENGTH: 305
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Query Match 85.4%; Score 35; DB 15; Length 305; Best Local Similarity 100.0%; Pred. No. 1e+02; Matches 6; Conservative 0; Mismatches 0; Indels
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CURRENT PILING DATE: 2003-01-06

FRIOR PAPLICATION NUMBER: US60/318,120

PRIOR PILING DATE: 2001-09-01

PRIOR PELING DATE: 2001-09-10

PRIOR PAPLICATION NUMBER: US60/318,430

PRIOR PELING DATE: 2001-09-17

PRIOR APPLICATION NUMBER: US60/361,63

PRIOR APPLICATION NUMBER: US60/396,412

PRIOR APPLICATION NUMBER: US60/396,412

PRIOR PELING DATE: 2001-09-17

PRIOR PELING DATE: 2001-09-19

PRIOR PELING DATE: 2001-09-19
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Publication No. US20040126762A1

GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: 52945201000

CURRENT APPLICATION NUMBER: US/10/322,281

CURRENT FILING DATE: 2002-12-17

NUMBER OF SEQ ID NOS: 866

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 857

LENGTH: 1071

TYPE: PRT

ORGANISM: Mus musculus
US-10-322-281-857
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85.7%; Pred. No. 3.6e+02;
tive 0; Mismatches 1; Indels (
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity
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US-10-236-417-158
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US-10-322-281-857
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Publication No. US20040048256A1

### GENERAL INFORMATION:

TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

### FILE REPRENCE: 2.1402-442C

CURRENT APPLICATION NUMBER: US/10/236,417

CURRENT FILING DATE: 2003-01-06

### PRIOR APPLICATION NUMBER: US60/318,120

### PRIOR APPLICATION NUMBER: US60/318,430

### PRIOR APPLICATION NUMBER: US60/318,430

### PRIOR APPLICATION NUMBER: US60/322,781

### PRIOR APPLICATION NUMBER: US60/322,781

### PRIOR PILING DATE: 2001-09-17

### PRIOR PILING DATE: 2001-09-17

### PRIOR PILING DATE: 2002-03-05

### PRIOR PILING DATE: 2002-03-05

### PRIOR APPLICATION NUMBER: US60/326,412

### PRIOR PILING DATE: 2002-03-05

### PRIOR PILING DATE: 2002-03-05

### PRIOR PILING DATE: 2001-09-17

#### PRIOR PILING DATE: 2001-09-17
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0; Indels
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PRIOR FILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 174
SOFTWARE: CuraSeqList version 0.1
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                TYPE: PRT
CORGANISM: Homo sapiens
US-10-041-615-2
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220 HRPLDK 225
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SEQ ID NO 156
LENGTH: 1052
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US-10-236-417-156
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US-10-236-417-164
                                                                                                  SEQ ID NO 2
LENGTH: 305
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Sequence 5, Application US/09799875 Patent No. US20020034780A1
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GENERAL INFORMATION:

APPLICANT: Agee et al.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-442C
CURRENT APPLICATION NUMBER: US/10/236,417
CURRENT APPLICATION NUMBER: US60/318,120
PRIOR PILING DATE: 2001-09-10
PRIOR PILING DATE: 2001-09-10
PRIOR PLICATION NUMBER: US60/318,430
PRIOR PLICATION NUMBER: US60/318,184
PRIOR PILING DATE: 2001-09-10
PRIOR PLICATION NUMBER: US60/318,184
PRIOR FILING DATE: 2001-09-07
PRIOR PLICATION NUMBER: US60/318,184
PRIOR PLILING DATE: 2001-09-07
PRIOR PLILING DATE: 2001-09-07
PRIOR PLILING DATE: 2002-07-17
PRIOR PLILING DATE: 2002-07-17
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PRIOR PLILING DATE: 2001-09-19
PRIOR PLILING DATE: 2001-09-19
PRIOR PLILING DATE: 2001-09-19
PRIOR PLILING DATE: 2001-09-19
PRIOR PRILING DATE: 2001-09-19
PRIOR PRING PRIOR DATE: 2001-09-19
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| Sequence 860, Application US/10322281
| Publication No. US20040126762A1
| Publication No. US20040126762A1
| GENERAL INFORMATION
| APPLICANT: David W. Morris
| APPLICANT: David W. Morris
| APPLICANT: Marc S. Malandro
| TITLE OF INVENTION: Novel Compositions and Methods in Cancer FILE REFERENCE: 529452001000
| CURRENT APPLICANTION NOVER: US/10/322,281
| CURRENT FILING DAYE: 2002-12-17
| NUMBER OF SEQ ID NOS: 866
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 860
| LENGTH: 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 35; DB 15; Length 1112;
Pred. No. 3.7e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.4%; Score 35; DB 16; Length 1182;
85.7%; Pred. No. 4e+02;
iive 0; Mismatches 1; Indels
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-10-236-417-158
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718 GHRPLSK 724
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Best Local Similarity
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SEQ ID NO 158
LENGTH: 1112
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RESULT 32

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GENERAL INFORMATION:
APPLICANT: Meyers, Rachel
TITLE OF INVENTION: No. US20020034780Alel Human Protein Kinases and Uses
TITLE OF INVENTION: Therefor
TITLE OF INVENTION: Therefor
FILE REPERENCE: 35800/20996
CURRENT APPLICATION NUMBER: US/09/799, 875
CURRENT APPLICATION NUMBER: 00/182,059
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-09-12
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 5:
LENGTH: 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Meyers, Rachel
APPLICANT: Meyers, Rachel
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Williamson, Mark
TITLE OF INVENTION: UNack
TITLE OF INVENTION: Therefor
TITLE OF INVENTION: Therefor
FILE REFERENCE: 3500/20996
CURRENT APPLICATION NUMBER: US/10/649,156
CURRENT APPLICATION NUMBER: US/09/799,875
PRIOR FILING DATE: 2001-03-06
PRIOR PILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/182,059
PRIOR PILING DATE: 2000-09-12
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 1203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35; DB 9; Length 1203;
Pred. No. 4e+02;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/10649156 Publication No. US20040038346A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 85.4%;
Best Local Similarity 85.7%;
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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US-10-236-417-160
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Gaps

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PRIOR FILING DATE: 2001-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
                                                                                                                                                                                                                                                                                                                                  Score 35; DB 15; Length 1321; Pred. No. 4.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1369;
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US-10-288-798-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: WALLEA, Narinder K.; HAFALLA, April J.A.;
APPLICANT: YAO, Monique G.; GANDHI, Ameena R.;
APPLICANT: GURURALAN, Rajagopal; Li;
APPLICANT: PATTERSON, Chandra; YUE, Li;
APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;
APPLICANT: THORNTON, Michaell, ELLIOTT, Vicki S.;
APPLICANT: THORNTON, Michaell, ELLIOTT, Vicki S.;
APPLICANT: AU-YOUNG, Janice; TANG, Y. Tom;
APPLICANT: AZIMZAI, Yalda; BURRIL, John D.;
APPLICANT: AZIMZAI, Yalda; BURRIL, John D.;
APPLICANT: KARWEW, Jana, POLICKY, Jenice L.;
APPLICANT: KRANEY, Liam; POLICKY, Jennifer L.;
APPLICANT: THANGAVELU, KAVITHA, BURFORD, Neil
TITLE OF INVENTION: HUMAN KINASES
CURRENT APPLICANT: CONTRACT POLICEY, Jenice L.;
FILE REFERENCE: PI-0209 USA
CURRENT FILING DATE: 2002-11-01
                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
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85.7%; Pred. No. 4.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Publication No. US20030207299A1
GENERAL INFORWATION:
APPLICANT: BANDMAN, Olga; NGUYEN, Danniel B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/10288798
Publication No. US20030207299A1
                                                                                                                                                                                                                                                                                                                                         85.4%;
85.7%;
                                                         Remaining Prior Application
NUMBER OF SEQ ID NOS: 341
SOFTWARE: Custom
SEQ ID NO 162
LENGTH: 1321
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 85.7
Matches 6; Conservative
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                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               857 CHRPLSK 863
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GHRPLDK 7
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                                                                                                                                                                                                                      TYPE: PRT
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GENERAL INFORMATION:

APPLICANT: Agee et al.

TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REPERENCE: 21402-442C
CURRENT APPLICATION NUMBER: US6/236,417
CURRENT APPLICATION NUMBER: US6/318,120
PRIOR PILING DATE: 2001-09-01
PRIOR PILING DATE: 2001-09-10
PRIOR PILING DATE: 2001-09-10
PRIOR PILING DATE: 2001-09-17
PRIOR PILING DATE: 2001-09-17
PRIOR PILING DATE: 2001-09-17
PRIOR PILING DATE: 2001-09-17
PRIOR PILING DATE: 2001-09-07
PRIOR PILING DATE: 2001-09-07
PRIOR PILING DATE: 2001-09-07
PRIOR PILING DATE: 2002-03-05
PRIOR PILING DATE: 2002-07-17
PRIOR PILING DATE: 2001-09-17
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TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REPERBERE: 21402-442C
CURRENT APPLICATION NUMBER: US/10/236,417
CURRENT FILING DATE: 2003-01-06
FRIOR PEDLICATION NUMBER: US60/318,120
PRIOR PELLONG DATE: 2001-09-10
PRIOR PELLONG DATE: 2001-09-10
PRIOR APPLICATION NUMBER: US60/318,430
FRIOR APPLICATION NUMBER: US60/318,430
FRIOR APPLICATION NUMBER: US60/312,781
PRIOR APPLICATION NUMBER: US60/312,781
PRIOR PILING DATE: 2001-09-17
FRIOR PILING DATE: 2001-09-17
FRIOR PILING DATE: 2001-09-17
FRIOR PILING DATE: 2002-03-05
FRIOR APPLICATION NUMBER: US60/361,663
FRIOR APPLICATION NUMBER: US60/322,636
FRIOR PILING DATE: 2001-09-17
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Publication No. US20040048256Al
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       809 GHRPLSK 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Custom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-236-417-160
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LENGTH: 1273
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Gaps

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FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(60)
OTHER INFORMATION: unsure at all Xaa locations
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85.7%; Pred. No. 66;
iive 0; Mismatches
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Best Local Similarity 85.7-
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Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Oryza Bativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          || |:||
46 GHSPMDK 52
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85.7%; Pred. No. 4.6e+02;
tive 0; Mismatches 1; IndelB
                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: NGUTES, Danniel B.; WALIA, Narinder K.
APPLICANT: NGUTES, Danniel B.; WALIA, Narinder K.
APPLICANT: GANDHI, Ameia B.; WALIA, Narinder G.
APPLICANT: GANDHI, Ameia B.; WALIA, Nariader B.
APPLICANT: DING, Li; PATTERSON, Chandra S.
APPLICANT: TYE, Henry; BANGHTH, Wariah R.
APPLICANT: TRIBOULEY, Catherine M.; THORNTON, Michael B.
APPLICANT: TRIBOULEY, Vicki S.; LU, Yan
APPLICANT: ELLIOTT, Vicki S.; LU, Yan
APPLICANT: BURRILL, John D.; MARCUS, Gregory A.
APPLICANT: BURREN, Bridget A.; KRARNEY, Liam
APPLICANT: BURRORD, Neil
APPLICANTORD, NEIL
APPLICANT: BURRORD, Neil
APPLICANTORD, NEIL
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APPLICANTORD, NEIL
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; OTHER INFORMATION: Incyte ID No. US20040038881A1 1989319CD1
US-10-362-892-7
                                                                                                                                                                                                          ; Sequence 7, Application US/10362892; Publication No. US20040038881A1; GENERAL INFORMATION:
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Best Local Similarity 85.7
Matches 6; Conservative
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ORGANISM: Homo sapiens
                                                      905 GHRPLSK 911
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; Sequence 183296, Application US/10437963; Publication No. US20040123343A1; GENERAL INFORMATION:

RESULT 38 US-10-437-963-183296

APPLICANT: La Rosa, Thomas J.

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, APPLICANT: Boukharov, Andrey A.;
APPLICANT: Barbazuk, Brad
; APPLICANT: Barbazuk, Brad
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: 1919118
; FILE REPERENCE: 38-21 (53221)8
; CURRENT PAPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; EMOUNTH: 60
; TYDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 236642, Application US/10424599
; Sequence 236642, Application WS/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
APPLICANT: Covalic David K
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: 10424,599
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT PILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 236642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.5%; Score 33; DB 16; Length 60; 71.4%; Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT3847_55714C.1.pep
US-10-424-599-236642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Clone ID: PAT_MRT4530_80400C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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APPLICANT: La Rosa Thomas J; APPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-424-599-240543
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## APPLICANT: Zhou Yihua

### APPLICANT: Cao Yongwel

### TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With

### TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

### FILE REPERENCE: 38-21(53223)

### CURRENT APPLICATION NUMBER: US/10/424,599

### CURRENT PELING DATE: 2003-04-28

### MUMBER OF SEQ ID NOS: 285684

### LENGTH: 157

### CURRENT PELING DATE: 2003-04-28

### CORGANISM: Glycine max

### PRATURE:

### ORGANISM: Glycine max

### PRATURE:

### COCATION: (1)...(157)

### COCATION: (1)...(157)

### COCATION: (1)...(157)

### COCATION: (1)...(157)

### COTHER INFORMATION: Clone ID: PAT_MRT3847_59238C.1.pep
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80.5%; Score 33; DB 15; Length 157;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels
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Search completed: June 1, 2005, 11:57:09 Job time: 87.2667 secs

||:||| 100 GHKPLD 105

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Thu Jun

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein 1, 2005, 11:41:15; Search time 22.4 Seconds (without alignments) 30.068 Million cell updates/sec June Run on:

US-09-424-940A-1 Title: Perfect score:

GHRPLDK 7 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB 8 Maximum DB 8 Maximum Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pIR 79:*
1: pir1:*
2: pir2:*
1: pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

myelin basic prote myelin basic prote hypothetical prote protein T17H7.16 [hypothetical prote probable WD-40-rep hypothetical prote pyroglutamyl-pepti hypothetical prote probable ATP-bindi fibrinogen beta ch probable transcrip fibrinogen beta ch zinc finger protei hypothetical prote fibrinogen beta ch multi resistance p fibrinogen beta ch ankyrin-like prote hypothetical prote prote prote prote probable oxidoredu queuine tRNA-ribos acyl-CoA synthase MutT/nudix family hypothetical hypothetical hypothetical hypothetical Description SUMMARIES 747840 738463 7846017 7846017 7846017 7846017 7846017 786017 786017 786017 786017 786017 786017 786017 786017 786017 786017 786017 786017 786017 786017 786017 786017 FGHUB C95399 FGBOB T46417 T19389 E71149 H87710 D96011 S77072 C69077 В Query Match Length 463 673 795 225 1058 423 42 169 169 176 215 Score Result

probable fadD36 pr proly1-tRNA synthe proly1-tRNA ligas cytidine/deoxycyti ipaA protein - Shi probable oxidoredu myoblast city prot CDA peptide synthe insulin 2 - toadfi hypothetical prote hypothetical prote	probable prosphe homectic protein A queuine tRNA-ribos hypothetical prote
G70607 G75072 A71093 A71093 E31265 C83023 C83023 INTO2 INTO2 H83530 H83530 G95291	E87094 A37041 AE3377 T35433
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473 480 480 548 633 633 1970 3670 104 1123	162 184 202 213
77.22.26.66.66.66.66.66.66.66.66.66.66.66.	73.2
	0000
33 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5

ALIGNMENTS

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Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfic
fibrinogen beta chain - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Accession: B94308; A03123; A37212; A05297; B37512; D03118
R;Birken, S.; Wilner, G.D.; Canfield, R.E.
Throndb. Res. 7, 599-610, 1975
A;Title: Studies of the structure of canine fibrinogen.
A;Reference number: A94308; MUID:76081726; PMID:1198547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Keywords: blood coagulation; liver; plasma; sulfoprotein
F;1-19/Product: fibrinopeptide B #status experimental <APT>
F;2/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
F;3/Binding site: sulfate (Tyr) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: A03118
A;Accession: A03123
A;Molecule type: protein
A;Residues: 1-19 BBLO-
R;Krajewski, T.; Blomback, B.
Acta Chem. Scand. 22, 1339-1346, 1968
A;Reference number: A37512; MUID:69066367; PMID:5727635
                                                                                                                                                                                                                                                                                                   A;Accession: B94308
A;Molecule type: protein
A;Residues: 1-31 <BIR>
A;Cross-references: UNIPROT:P02677
R;Blombaeck, B.; Blombaeck, M.; Groendahl, N.J.
Acta Chem. Scand. 19, 1789-1791, 1965
A;Tille: Studies on fibrinopeptides from mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A37512
A; Molecule type: protein
A; Residues: 1-19 < KRA>
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Length 31;

Gaps ö ; Score 41; DB 2; Length 31; Pred. No. 0.057; 0; Mismatches 0; Indels 100.0%; Query Match 100. Best Local Similarity 100. Matches 7; Conservative

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GHRPLDK 26 GHRPLDK 7 20 셤 δ

RESULT 2

fibrinogen beta chain precursor [validated] - human

N;Alternate names: coagulation factor I
N;Contains: fibrinopeptide B
C;Species: Homo sapiens (man)
C;Apecies: 4-Apr-1984 #sequence revision 31-Mar-1993 #text change 09-Jul-2004
C;Accession: B43568; A90469; B90469; I37389; A94433; A90437; A94309; G54223; A03121; B371
R;Chung, D.W.; Harris, J.E.; Davie, E.W.
Adv. Exp. Med. Biol. 281, 39-48, 1990

thiamin biosynthes

us-09-424-940a-1.rpr

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R;Kirschbaum, N.E.; Budzynski, A.Z.
J. Biol. Chem. 265, 13669-13676, 1990
A;Title: A unique proteolytic fragment of human fibrinogen containing the Aalpha COOH-ter
A;Reference number: A37117; WUID:90337977; PMID:2143188
A;Contents: annotation; hementin cleavage site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Note: hementin, a protease from Haementeria ghilianii, the giant South American leech, C; Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves ization sites responsible for the formation of the soft clot.

G; Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabiliz ger) and between alpha chains (weaker) of different monomers.

C; Comment: All fibrinogen chains are synthesized in the liver.
    Annu. Rev. Biochem. 53, 195-229, 1984

A;Title: Fibrinogen and fibrin.
A;Reference number: A50041; MUID:84305751; PMID:6383194
A;Contents: annotation; review, Bs structure, polymerization, ligands R;Chung, D.W.; Rixon, M.W.; Que, B.G.; Davie, E.W.
Ann. N. Y. Acad. Sci. 408, 449-456, 1983
A;Title: Cloning of fibrinogen genes and their cDNA.
A;Feterence number: A50038; MUID:83254384; PMID:6575700
A;Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: GDB:119130; OMIM:134830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45 GHRPLDK 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
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Attenders 1-31 (HBL)
Attenders 1-31 (HBL)
Attenders 1-34 (HBBL)
Attenders 1-
                                                                                                                                                                                                                                                                                                                                              A;Tills: Characterization of complementary deoxyribonucleic acid and genomic deoxyribonu A;Reference number: A90469; MUID:83283433; PMID:6688356
A;Accession: A90469
A;Residues: 1-38 cCH1>
A;Residues: 1-38 cCH1>
A;Accession: B90469
A;Accession: B90469
A;Accession: B90469
A;Residues: 9-191,'A', 193-491 cCH2>
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R;Doolittle, R.F.; Takagi, T.; Watt, K.; Bouma III, H.; Cottrell, B.A.; Cassman, K.G.; G
R;Doolittle, R.F.; Takagi, T.; Watt, K.; Bouma III, H.; Cottrell, B.A.; Cassman, K.G.; G
A; Title: The structures of fibrinogen and fibrin.
A;Reference number: A94437
A;Contents: annotation; disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:J00129; NID:g182429; PIDN:AAA52429.1; PID:g182430
R;Huber, P.; Dalmon, J.; Courtois, G.; Laurent, M.; Assouline, Z.; Marguerie, G.
Nucleic Acids Res. 15, 1615-1625, 1987
A;Title: Characterization of the 5'-flanking region for the human fibrinogen beta gene.
A;Reference number: I37389; MUD:87146483; PMID:3029722
A;Accession: I37389
A;Status: translated from GB/EMBL/DDBJ
A;Residues: 1-38 <HUBs
A;Title: Nucleotide sequences of the three genes coding for human fibrinogen. A;Reference number: A43568; MUID:91344740; PMID:2102623
                                                                                                                                                                                                                       A, Cross-references: UNIPROT: P02675
K; Chung, D.W.; Que, B.G.; Rixon, M.W.; Mace Jr., M.; Davie, E.W.
Biochemistry 22, 3244-3250, 1983
A, Title: Characterization of complementary deoxyribonucleic acid
                                                                                           A,Accession: B43568
A,Molecule type: DNA
A,Residues: 9-191,'P',193-491 <CHU>
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A Map position: 4q28-4q28 Aintrons: 38/3; 102/3; 14/1; 240/1; 278/1; 320/1; 415/2 Aintrons: 38/3; 102/3; 14/1; 240/1; 278/1; 320/1; 415/2 Longlex: The fibringen molecule is a hexamer containing two sets of alpha (see PIR:FGI ins are contained in the core. Two three-chain colled coils emerge from this core and confirm the distal domain nodes.
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Lyburd
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C,Species: Sinorhizobium meliloti
C,Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C,Accession: C95399
R,Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse
F,Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse
F, Kahman, S.; Keating, D.H.; Palh, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.;
Fro. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A; Fitle: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
A; Reference number: A95262; MUID:21396509; PMID:11481432
A; Accession: C95399
A; Accession: C95399
A; Molecule type: DNA
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Gaps

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C;Accession: T47840
R;Nyakatura, G;Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.; Submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24475
A;Accession: T47840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Riweissbach, L.; Oddoux, C.; Procyk, R.; Grieninger, G.
Biochemistry 30, 3290-3294, 1991
A;Title: The beta chain of chicken fibrinogen contains an atypical thrombin cleavage sit
A;Reference number: A38463; MUID:91182745; PMID:2009266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: UNIPROT:Q02020, GB:M58514; NID:g211779; PIDN:AAA48770.1; PID:g211780 CS.Querfemanily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfise F;73-202/Domain: fibrinogen disulfide ring homology «FBR» F;212-460/Domain: fibrinogen beta/gamma homology «FBG»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 3
A;Introns: 9/1; 795/3; 824/3; 1036/3; 1075/3; 1174/1; 1245/3; 1347/3; 1369/1; 1449/1
A;Note: T209.140
C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fibrinogen beta chain - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental F;6/Binding site: sulfate (Tyr) (covalent) #status experimental $2:1-22/Cleavage site: Arg-Gly (thrombin) #status experimental F;371/Binding site: carbohydrate (Asn) (covalent) #status predicted F;372-373/Cleavage site: Arg-Thr (plasmin) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1490 «NYA»
A;Cross-references: UNIPROT:Q9M1C7; EMBL:AL138658
A;Experimental source: cultivar Columbia; BAC clone T209
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                multi resistance protein homolog - Arabidopsis thaliana
                                                                                                                                                                                               Score 36; DB 1;
Pred. No. 12;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N;Alternate names: protein T209.140
                                                                                                                                                                                                                             85.78;
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Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                              6; Conservative
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Best Local Similarity
Matches 6; Conserv
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A;Status: preliminary
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                             A;Cross-references: UNIPROT:092XY9; GB:AE006469; PIDN:AAK65757.1; PID:g14524255; GSPDB:GA;Rxperimental source: strain 1021, megaplasmid pSymA
R;Galibert, P.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, A;Authors: Kahn, D.; Rahn, M.L.; Ralman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Residues: 5-21 csJo.
R; Residues: 5-21 csJo.
R; Martinelli, R.A.; Inglis, A.S.; Rubira, M.R.; Hageman, T.C.; Hurrell, J.G.R.; Leach, S Arch. Biochem. Biophys. 192, 27-32, 1979
A; Title: Amino acid sequences of portions of the alpha and beta chains of bovine fibrinc A; Reference number: A37507; MUID:79164394; PMID:434821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Mesidues: 373-374 <MED>
A; Residues: 373-374 <MED>
C; Comment: Thrombin cleaves the bond between Arg-21 and Gly-22 to release fibrinopeptide
C; Comment: Fibrinogen is a hexamer containing two sets of three nonidentical chains (alp
C; Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfi
C; Reywords: blood coaquiation; alycoprotein; plasma; pyroglutamic acid; sulfoprotein
F; 76-205/Domain: fibrinogen disulfide ring homology <PDR>
F; 715-464/Domain: fibrinogen beta/gamma homology <PBG>
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A; Residues: 22-53 <MAR>
R; Chung, D.W.; Rixon, M.W.; MacGillivray, R.T.A.; Davie, E.W.
R; Chung, D.W.; Rixon, W.W.; MacGillivray, R.T.A.; Davie, E.W.
A; Title: Characterization of a cDNA clone codding for the beta chain of bovine fibrinogen
A; Reference number: A37513; MUID: 81199473; PMID: 6262803
A; Accession: A37513
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R;Medved, L.V.; Platonova, T.N.; Litvinovich, S.V.; Lukinova, N.I.
R;Medved, L.V.; Platonova, T.N.; Litvinovich, S.V.; Lukinova, N.I.
A;Title: The cleavage of beta-chain in bovine fibrinogen D(H) fragment (95 kDa) leads to A;Reference number: S02443; MUID:88211875; PMID:2966748
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C;Species: Bos primiqenius taurus (cattle)
C;Accession: 303122; B03117; B37507; A37513; S02443
R;Blomback, B.; Doolittle, R.F.
Acta Chem. Scand. 17, 1816-1819, 1963
A;Title: The sequence of amino acids at the N-terminal end of bovine fibrinopeptide A;Reference number: A03122
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A; Residues: 1-4 <BLO>
R; Sjoquist, J; Blomback, B.; Wallen, P.
Ark. Kemi 16, 425-436, 1960
A; Title: Amino acid sequence of bovine fibrinopeptides.
A; Reference number: A03117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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Pred. No.
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175 GHRPLD 180
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: SMa2008
A;Genome: plasmid
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A,Status: preliminary
A,Molecule type: DNA
A,Molecule type: DNA
A,Fesidues: 1-225 <WHI>
A,Cross-references: UNIPROT:Q9RXW3; GB:AE001881; GB:AE000513; NID:g6457853; PIDN:AAF09775
C,Genetics:
A,Gene: DR0192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: D82654
S;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequence Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: D82654
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A;Residues: 1-1058 <SIM>
A;Cross-references: UNIPROT:Q9PCW4; GB:AE003991; GB:AE003849; NID:g9106696; PIDN:AAF84449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Experimental Source: strain 9a5c
R;Simpson, A.J.G; Reinach, P.C; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; All Briones, M.R.S.; Bueno, M.R.D.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H as Neco., E.; Docena, C.; Bl-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre chado, M.A.; Madeira, M.M.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.C.; de Oliveira, M.C.; de Oliveira, M.C.; de Oliveira, M.C.; de Sa, R.G.; Santelli, R.V.; Sawaeah, A;Reference number: A59328
A;Reference number: A59328
A;Contents: annotation
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T20233
R;Wilkinson, J.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19241
A;Reference number: Z19241
A;Accession: T20333
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                  Length 225;
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Pred. No. 1.2e+02;
1; Mismatches 0;
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Pred. No. 23;
0; Mismatches
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83.3%;
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C; Superfamily: NUDIX hydrolase
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Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 85.7
Matches 6; Conservative
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A;Gene: XF1640
                                                                                                                                                                                                                                                                                                                     Query Match
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C. Species: Arabidopsis thaliana (mouse-ear cress)  
C. Species: Arabidopsis thaliana (mouse-ear cress)  
C. Species: Arabidopsis thaliana (mouse-ear cress)  
C. Accession: A84608  
R. Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, L. Nature 402, 761-768, 1999  
A. Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A. Reference number: A84420; MUD:20083487; PMID:10617197  
A. Accession: A8608  
A. Status: preliminary  
A. Molecule type: DNA  
A. Molecule type: DNA  
A. Molecule type: DNA  
A. Consolar Eferences: UNIPROT:09SIZ7; GB:AE002093; NID:94417294; PIDN:AAD20419.1; GSPDB:GN
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A.5550
MutT/nudix family protein - Deinococcus radiodurans (strain R1)
C.Species: Deinococcus radiodurans
C.Species: Deinococcus radiodurans
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C.Accession: A7550
C.Accession: A7550
C.Accession: A7550
M.; Shen, M.; Vanathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma S. Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A.Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75550; MuID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:094271; EMBL:AL032684; PIDN:CAA21808.1; GSPDB:GN00067; SPDB:
A;Experimental source: strain 972h-; clone pl p8B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                Zinc finger protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T40817
R;Beck, A.; Reinhardt, R.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
Bubmitted to the EMBL Data Library, October 1998
A;Reference number: Z21949
A;Accession: T40817
A;Atcession: T40817
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: DABA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 82.9%; Score 34; DB 2; Length 673; Local Similarity 71.4%; Pred. No. 46; 1; Indels es 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 795;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 2
F;210-278/Domain: RING finger homology <RRN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 GHHPMDK 166
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                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-673 <BEC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: SPDB: SPBP8B7.23
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: At2g22020
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Rilin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N'Alternate names: myelin Al protein
C'Species: Oryccolagus cuniculus (domestic rabbit)
C'Date: 30-Sep-1991 #esquence_revision 30-Sep-1991 #text_change 30-Sep-1993
C'Accession: B92087; A03140
C'Accession: B92087; A03140
R'Shapira, K.; McKrachally, S.S.; Chou, F.; Kibler, R.F.
A'Bhapira, K.; McKrachally, S.S.; And, By All Ayritle: Encephalitogenic fragment of myelin basic protein. Amino acid sequence of bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q9ZU34; GB:AE002093; NID:g4262240; PIDN:AAD14533.1; GSPDB:GN(
                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T17245
R;Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, September 1999
A;Reference number: Z18722
                                                                                                                                                                                                                      probable WD-40-repeat protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004 C;Accession: D84423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 32; DB 2; Length 878;
Pred. No. 1.6e+02;
1; Mismatches 1; Indels
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Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: adult uterus; clone DKFZp586J0917 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein DKFZp586J0917.1 - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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83.3%;
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Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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403 GHRPLSR 409
                                                                     18 GDRPLDK 24
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408 GHOPLD 413
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A; Residues: 1-611 <STO>
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A;Residues: 1-878 <KOE>
                               1 GHRPLDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
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A;Gene: At2g01330
A;Map position: 2
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Cispectes: Mycobacterium leprae
Cispectes: Mycobacterium leprae
Cipate: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
CiAccession: E87040
R; Davies, R. T. Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R; Davies, R. T. Butherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A66909; MulD:21128732; PMID:11234002
A;Accession: E87040
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A;Residues: 1-485 <AQP>
A;Cross-references: UNIPROT:O67746; GB:AE000763; NID:G2984178; PIDN:AAC07717.1; PID:G298
A;Experimental source: strain VP5
                       A;Residues: 1-423 <WIL>
A;Cross-references: UNIPROT:Q18847; EMBL:Z75533; PIDN:CAA99815.1; GSPDB:GN00019; CESP:C5
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A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: F70464
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C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: F70464
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                                                                                                        C,Genetics:
A,Gene: CESP.C54G4.2
A,Map position: 1
A,Introns: 76/3; 172/3; 272/2; 312/1; 367/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C54G4.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: xclC
C;Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology
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Pred. No. 83;
3; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                       Query Match 78.0%; Score 32; DB 2; Length 423; Best Local Similarity 83.3%; Pred. No. 73; Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
E87040
acyl-CoA synthase [imported] - Mycobacterium leprae
                                                                                 A; Experimental source: clone C54G4
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Similarity 57.1%;
4; Conservative
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197 HRPLDR 202
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                                                                                                                                                                                                                                                                                                                                                                                         2 HRPLDK 7
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                                                                                                     Genetics:
Gene: CESP:C54G4.2
A; Molecule type: DNA
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A,Gene: aq 1912
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A;Reference number: A94241, MUID:70178977; PMID:5442707
A;Contents: annotation
A;Contents: annotation
A;Contents: annotation
A;Contents: annotation
C;Robe: the region including residues 114-122 induces experimental allergic encephalomyel
C;Superfamily: myelin basic protein
C;Reywords: acetylated amino end; amidated carboxyl end; experimental autoimmune encephal
F;1-16/Product: myelin peptide amide-16 #status experimental cPA16-
F;1-116/Product: myelin peptide amide-16 #status experimental cPA16-
F;1-Modified site: acetylated amino end (Ala) #status experimental
F;12/Modified site: amidated carboxyl end (Tyr) (amide in mature form myelin peptide amic
F;16/Modified site: amidated carboxyl end (Ala) (amide in mature form myelin peptide amic
F;106/Modified site: omega-N-methylarginine or omega-N'omega-N'-dimethylarginine (Arg) (§
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kn DNA Res. 6, 83-101, 1999
A;Fitle: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrn A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-169 «KAW»
A;Cross-references: UNIPROT:Q9Y9B8; DDBJ:AP000064; NID:g5105945; PIDN:BAA81382.1; PID:g53|
A;Experimental source: strain Kl
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Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C. A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I A;Authors: Squence and analysis of chromosome 1 of the plant Arabidopsis.
A;Feference number: A86141; MUID:21016719; PMID:11130712
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: F72465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 31; DB 1; Length 169;
Pred. No. 44;
1; Mismatches 1; Indels
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Pred. No. 44;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity 71.4%;
Matches 5; Conservative
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76 GHRPQDE 82
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A;Molecule type: DNA
A;Residues: 1-176 <STO>
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A.Molecule type: protein
A.Molecule type: Drotein
A.Residues: 1,'S',2-169 eETL>
A.Cross-references: UNIPROT: P02687
B.Brostoff, S.W.; Reuter, W.; Hichens, M.; Eylar, E.H.
B.Brostoff, S.W.; Reuter, W.; Hichens, M.; Eylar, E.H.
B.Title: Specific cleavage of the Al protein from myelin with cathepsin D.
A.Reference number: A92160; MUID: 74070688; PMID: 4129204
A.Accession: A92160
A.Molecule type: protein
B.Residues: 1-169 eBRO>
B.S.; Chou, F.; Kibler, R.F.
J. Biol. Chem. 246, 4630-4640, 1971
A.Title: Encephalitogenic fragment of myelin basic protein. Amino acid sequence of bovin
A.Reference number: A92087
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Ajaccesion: J. 306, 551-555, 1995
Ajaccesion: S54343; MUID:95194333; PMID:7887910
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A; Residues: 74-75, 'HG', 78-82,'D', 84-88;105,'X',107-108,'X',110-114,'X',116-119 <OKA>
R; Takamatsu, K.; Tatemoto, K.
Neurochem. Res. 17, 239-246, 1992
A;Title: Isolation and characterization of two novel peptide amides originating from mye A; Reference number: A61641; MUID:92319189; PMID:1377792
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A.Residues: 1-16 < CTA2.
A.Residues: 1-16 < CTA2.
A.Note: these peptides have carboxyl-terminal amides probably produced by a non-enzymati
R.Brostoff, S.; Eylar, E.H.
B.P.C.: Natl. Acad. Sci. U.S.A. 68, 765-769, 1971
A.Title: Localization of methylated arginine in the Al protein from myelin.
A.Reference number: A93777; MUID:71153946; PMID:4994464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MyAlternate names: myelin Al protein
NyAlternate names: myelin Al protein
NyAlternate names: myelin Al protein
NyContains: myelin peptide amide-12 (MPA-12); myelin peptide amide-16 (MPA-16)
Cypecies: Bos primigenius taurus (cattle)
Cypecies: Bos primigenius taurus (cattle)
Cypate: 18-Dec-1981 #sequence revision 18-Dec-1981 #text change 09-Jul-2004
CyAccession: A92089; A92160; A92087; S54343; A61641; B61641; A03140
RiPAJAT, E.H.; Brostoff, S.; Hashim, G.; Caccam, J.; Burnett, P.
A; Hile: Baaic Al protein of the myelin membrane. The complete amino acid sequence.
A; Reference number: A92089; MUID:72007306; PMID:5096093
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    A;Reference number: A92087
A;Accession: B92087
A;Molecule type: protein
C;Superfamily: myelin basic protein
C;Keywords: myelin
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A;Residues: 1-12 <TAK>
A;Accession: B61641
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A, Residues: 1-215 < AWA>
A, Residues: 1-215 < AWA>
A, Experimental Bource: strain 168
A, Experimental Bource: strain 168
B, Kunst, F: Ogaswara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A, Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G; Kroph, S.; Kumano, M.; Kurita, Y.; Lapidus, A.; Lardinois, A, Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueell Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Saronlon, A, Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sekor, T.; Walthers: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, A, Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Vata, K.; Asumoto, K.; Yata, K.; Yoshida, M.; A; Title: The complete genome sequence of the Gram-Positive bacterium Bacillus subtilis.
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$23432
pyroglutamyl-peptidase I (EC 3.4.19.3) pcp - Bacillus subtilis
pyroglutamyl-peptidase I (EC 3.4.19.3) pcp - Bacillus subtilis
NiAlternate names: 5-oxoprolyl-peptidase; pyrrolidone-carboxylate peptidase pcp
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Accession: $23432; 669673
R;Awade, A.; Cleuziat, P.; Gonzales, T.; Robert-Baudouy, J.
FEBS Lett. 305, 67-73, 1992
A;Title: Characterization of the pcp gene encoding the pyrrolidone carboxyl peptidase of A;Reference number: $23432; MUID:92339527; PMID:1353026
A;Cross-references: UNIPROT:Q9SY30; GB:AE005172; NID:g4926831; PIDN:AAD32941.1; GSPDB:GN
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A, Cross-references: GB: Z99105, GB: AL009126, NID: g2632457, PIDN: CAB12059.1, PID: g2632551
A, Experimental source: strain 168
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C;Superfamily: pyrrolidone-carboxylate peptidase (N-terminal pyroglutamyl peptidase)
C;Keywords: hydrolase; omega peptidase
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25957
R;Wamsley, P.; Kramer, J.
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Pred. No. 58;
3; Mismatches 0; Indels
                                                                                                                                                          2; Length 176;
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57.1%;
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97 GHQPIDE 103
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Best Local Similarity
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GHKPINK 8
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                          C;Genetics:
A;Gene: T17H7.16
A;Map position: 1
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A; Molecule type: DNA
A; Reaidues: 1-225 <WAM>
A; Cross-references: UNIPROT:P91542; EMBL:U80839; PIDN:AAB37923.1; GSPDB:GN00020; CESP:ZC.
A; Experimental source: strain Bristol N2; clone ZC204
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Cibate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
Cibate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
Cibacession: D83071
Sibate: D8
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A;Experimental source: strain PAO1
C;Genetics:
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C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
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S;Blum, H.; Bauersachts, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23034
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Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 225;
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submitted to the EMBL Data Library, December 1996
A;Description: The sequence of C. elegans cosmid ZC204.
A;Reference number: Z20116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein DKFZp434K1323.1 - human (fragment)
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                                                                                                                                      A;Accession: T25957
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Cross-references: UNIPROT:Q9NSV7; EMBL:AL137714
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 2
A;Introns: 28/2; 55/3; 87/3; 133/1
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83.3%;
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83.3%;
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity
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A, Status: preliminary
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A; Status: preliminary
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R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.E. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolons n. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT;Q9A244; GB:AE005673; NID:g13425492; PIDN:AAK25684.1; GSPDB:GP:CJGenetics:
CJGenetics:
A;Gene: CCJ722
C;Superfamily: phosphoglycerate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable oxidoreductase protein SMb20648 [imported] - Sinorhizobium meliloti (strain 1021] C;Species: Sinorhizobium meliloti (c)Species: Sinorhizobium meliloti (c)Species: Sinorhizobium meliloti (c)Species: 24-Aug-2001 #text_change 09-Jul-2004 (c)Accession: D96011 R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernanc Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001 A;Filte: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endos A;Reference number: A95842; WUID:21396508; PMID:11481431
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A,Molecule type: DNA
A,Status: 1.345 < KURN>
A,Molecule type: DNA
A,Molecule type: DNA
A,Molecule type: DNA
A,Molecule type: DNA
A,Gross-references: UNIRROT:092TY7; GB:AL591985; FIDN:CAC49756.1; FID:g15141243; GSPDB:GR
A,Experimental source: strain 1021, megaplasmid pSymB
A,Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
Dela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
Science 293, 668-672, 2001
A,Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, B.; Komp, C.; Lelaure,
A,Authors: Kahn, D.; Kahn, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.(
A,Fitle: The composite genome of the legume symbiont Sinorhizobium meliloti.
A,Reference number: A96039; WuID:21368234; PMID:11474104
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C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S77072
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      queuine tRNA-ribosyltransferase (EC 2.4.2.29) - Synechocystis sp. (strain PCC 6803) N/Alternate names: protein slr0713; transfer RNA-guanine transglycosylase C;Species: Synechocystis sp.
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C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 31; DB
Pred. No. 95;
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Similarity 71.4%;
5; Conservative
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Best Local Similarity 71.4°
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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A,Molecule type: DNA
A,Residues: 1-344 <STO>
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B71149
hypothetical protein PH0407 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Accession: E71149
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a A;Reference number: A71000; MUID:98344137; PMID:9679194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q9XTZ2; EMBL:Z92826; PIDN:CAB07322.1; GSPDB:GN00021; CESP:C1
A;Experimental source: clone C18D11
C;Genetics:
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A; Note: this accession replaces an interim accession for a sequence replaced by GenBank C; Genetics:
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                                                                                                                                                                                                                                                                              hypothetical protein C18D11.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Aug-2004 C;Accession: T19389 #sequence_revision 15-Oct-1999 #text_change 16-Aug-2004 R;Barlow, K.

R;Barlow, K.

Barlow, K.

A;Reference number: Z19118
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H87710
hypothetical protein CC3722 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: H87710
               Gaps
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Pred. No. 95;
1; Mismatches 1; Indels
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               Indels
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-309 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 31; DB 2;
Pred. No. 85;
0; Mismatches 1
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C,Superfamily: ribonucleoprotein repeat homology
            1; Mismatches
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Best Local Similarity 83.3%;
Matches 5; Conservative
            5; Conservative
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                                                                                                                            HRPLDE 183
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Best Local Similarity
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                                                                    2 HRPLDK 7
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                                                                                                                                  178
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            Matches
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us-09-424-940a-1.rpr

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A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-473 <COL>
A;Cross-references: UNIPROT:005295; GB:Z93777; GB:AL123456; NID:g3261726; PIDN:CAB07836.. C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prolyl-tRNA synthetase (pros) PAB1724 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Species: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: G75072
C;Accession: G75072
C;Accession: G75072
C;Accession: G75072
Submitted to the EMBL Data Library, July 1999
A;Degcription: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struction:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Kawarabbyasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin: M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi DNA Res. S, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a-A;Reference number: A71000; MUID:98344137; PMID:9679194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-400 <KMW>
A; Cross-references: 1-401 (KMP)
A; Cross-references: 1.401 (MIPROT:058734; GB:AP000004; NID:g3236131; PIDN:BAA30103.1; PID:g325
A; Experimental source: strain OT3
A; Note: this accession replaces an interim accession for a sequence replaced by GenBank C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Cross-references: UNIPROT:Q9V022; GB:AJ248286; GB:AL096836; NID:g5458366; PIDN:CAB4988·
A,Experimental source: strain Orsay
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A;Molecule type: DNA
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C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Accession: A71093
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C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
                                                                                                                                                                                                                                                                                             A;Gene: FadD36
C;Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology
F;42-469/Domain: acetate-CoA ligase homology <ACL>
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Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 75.6%; Score 31; DB 2; Length 473
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 3; Mismatches 0; Indels
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83.3%;
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A, Accession: G75072
A, Status: preliminary
A, Molecule type: DNA
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Best Local Similarity
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    A; Accession: G70607
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A. Hacteriol. 179, 7135-7155, 1997
A. Hacteriol. C69070; MUID:98037514; PMID:9371463
A. Hacteriol. C69070; MUID:98037514; PMID:9371463
A. Hacteriol. C69070
A. Hacteriol. C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Offunction: catalyzes the exchange of guanine base in the first anticodon position of Afbatchion: catalyzes the exchange of guanine base in the first anticodon position of Afbatchway: queuosine biosynthesis; tRNA modification C;Superfamily: queuine tRNA-ribosyltransferase C;Keywords: glycosyltransferase; pentosyltransferase; tRNA modification
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probable fadD36 protein - Mycobacterium tuberculosis (strain H37RV)

probable fadD36 protein - Mycobacterium tuberculosis

probable fadD36 protein - Mycobacterium tuberculosis

C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C; Date: 18-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

Connor, R; Davies, R; Perkhill, J; Falvall, T; Gentles, S; Hamris, D; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 33, 537-544, 1998

A; Authors: Sqares, R; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                       A; Accession: S77072
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-374 < KAN>
A; Residues: 1-374 < KAN>
A; Cross-references: UNIPROT: 055983; EMBL: D64005; GB: AB001339; NID: g1001779; PIDN: BAA1076
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C; Genetics:
DNA Res. 3, 109-136, 1996
A,Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.6%; Score 31; DB 2; Length 374; 83.3%; Pred. No. 1e+02; ive 1; Mismatches 0; Indels
                                                                                                                             A; Reference number: S74322; MUID: 97061201; PMID: 8905231
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C, Superfamily: thiamin biosynthesis protein thiC
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Matches 5; Conservative
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GHMPLDQ 273
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A;Start codon: GTG
C;Function:
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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: C83023
A:Stcover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Asture 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog A;Reference number: A82950; MUD: 20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA A;Residues: 1-648 <STO> A;Cross-references: UNIPROT: Q9HUH9; GB:AE004911; GB:AE004091; NID:g9951264; PIDN:AAG083771 A;Experimental source: strain PAO1
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R,Saunder, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A submitted to the EMBL Data Library, March 1999
                                                                    probable oxidoreductase PA4986 [imported] - Pseudomonas aeruginosa (strain PAO1)
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C;Superfamily: Methylophilus methylotrophus W3A1 trimethylamine dehydrogenase
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A,Molecule type: mRMA
A,Residues: 1-1970 < ERI>
A,Cross-references: UNIPROT: Q9VCH4; EMBL:AF007805; NID:92367443; PID:92367444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   myoblast city protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C,Species: Streptomyces coelicolor
C,Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 12-Jul-2004
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Pred. No. 6.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: T03284
R;Erickson, M.R.S.; Galletta, B.J.; Abmayr, S.M.
J. Cell Biol. 138, 589-603, 1997
A;Title: Drosophila myoblast city encodes a conserved pr
A;Reference number: Z14881; MUID:97392689; PMID:9245788
A;Accession: T03284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 31; DB 2; Lei
Pred. No. 1.9e+02;
3; Mismatches 0;
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A;Molecule type: DNA
A;Residues: 1-3670 <SAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 75.6%;
Similarity 57.1%;
4; Conservative
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605 GHQPVDR 611
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490 GHQPIDE 496
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: C83023
A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 37
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                                                                                                                                                                                                                    RESULT 33
C75499
C75499
C75499
C75499
C75499
C75499
C75406
C.Species: Deinococcus radiodurans
C.Species: Deinococcus radiodurans
C.Species: Deinococcus radiodurans
C.Species: Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C.Accession: C75499
R.White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
K.M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Massidence 286, 1571-1577, 1999
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A.Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A.Reference number: A75250; MUID:20036896; PMID:10567266
A.Accession: C75499
A.Accession: C75
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A; Residues: 1-633 <VEN)
A; Residues: 1-633 <VEN)
A; Cross-references: UNIPROT: P18010; EMBL: X17628; NID: 947030; PIDN: CAA35624.1; PID: 947031
A; Cross-references: UNIPROT: P18010; EMBL: X17-9321, 1988
Proc. Natl. Acad. Sci. U.S.A. 85, 9317-9321, 1988
A; Title: Characterization of invasion plasmid antigen genes (ipaBCD) from Shigella flext A; Reference number: A94219; MUID: 89057927; PMID: 3057506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ipaa protein - Shigella flexneri plasmid
C.Species: Shigella flexneri
C.Species: Shigella flexneri
C.Jacession: S12763, Bsguence_revision 26-Apr-1996 #text_change 09-Jul-2004
C.Jacession: S12763, B31265
R.Venkatesan, M.M.; Buysse, J.M.
Nucleic Acids Res. 18, 1648, 1990
A.Title: Nucleotide sequence of invasion plasmid antigen gene ipaA from Shigella flexner
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      1; Indels
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Pred. No. 1.6e+02;
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Pred. No. 1.8e+02;
   0; Mismatches
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71.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Experimental source: strain R1 (5, Genetics: 8, Genetics: A;Gene: DR0603 A;Map position: 1
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Best Local Similarity 83.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 75.6
Best Local Similarity 71.4
Matches 5; Conservative
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    159 GHRPEDR 165
                                                                                                                       96 GHEPLD 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     417 GHRPLN 422
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                                                                    1 GHRPLD 6
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A;Molecule type: DNA
A;Residues: 1-88 <VE2>
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Matches
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us-09-424-940a-1.rpr

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Query Match
Best Local Similarity
Matches 5; Conserv
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A;Cross-references: UNIPROT:0924X5; EMBL:AL035640; PIDN:CAB38517.1; GSPDB:GN00070; SCOED A;Experimental source: strain A3(2)
C,Genetics:
A;Genetics:
A;Genetics:
C;Genetics:
C;Superfamily: non-ribosomal peptide synthetase; acetate-CoA ligase homology; acyl carric (5.8uperfamily: non-ribosomal peptide synthetase; phosphoprotein (5.8uperfamily: non-ribosomal peptide synthetase; phosphoprotein (5.8uperfamily: non-ribosomal peptide synthetase; phosphoprotein (5.8uperfamily: acetate-CoA ligase homology <ACL1>
F;512-932/Domain: acyl carrier protein homology <ACL2>
F;5948-1016/Domain: acyl carrier protein homology <ACL2>
F;597-1055/Domain: acetate-CoA ligase homology <ACL2>
F;2608-3064/Domain: acetate-CoA ligase homology <ACL3>
F;3080-3147/Domain: acyl carrier protein homology <ACL3>
F;3080-3112/Binding site: phosphopantetheine (Ser) (covalent) #status predicted
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H83530

H87530

H87530

H87530

H87530

H87540

C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000

G;Species: 15-Sep-2000

H87530

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Jature 406, 959-964, 2000
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A; Accession: H83530
A; Status: Perliminary
A; Molecule type: DNA
A; Residues: 1-104 <STO>
A; Cross-references: UNIPROT:Q91535; GB:AE004526; GB:AE004091; NID:g9946819; PIDN:AAG0431
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C;Species: Batrachoididae gen. sp. (toadfish)
C;bate: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 09-Jul-2004
C;Accession: A01605
R;Smith, L.F.
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A; Title: Species variation in the amino acid sequence of insulin.
A; Reference number: A90029; MUID:66160119; PMID:5949593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 75.6%; Score 31; DB 2; Length 3670; Best Local Similarity 83.3%; Pred. No. 1.2e+03; Matches 5; Conservative 0; Mismatches 1; Indels
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73.2%; Score 30; DB 1; Length 50;
Best Local Similarity 83.3%; Pred. No. 20;
Matches 5; Conservative 0; Mismatches 1; Indels
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A.Residues: 1-29;30-50 cSMI>
A.Cross-references: UNIPROT:P01338
C.Superfamily: insulin
C.Superfamily: insulin
C.Keywords: hormone; pancreas
F;1-29/00main: insulin chain B #status experimental cBCH>
F;1-29/30-50/Porduct: insulin #status experimental cACH>
F;30-50/Domain: insulin chain A #status experimental cACH>
F;8-36;20-49,35-40/Disulfide bonds: #status predicted
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C, Genetics:
A, Gene: PAO922
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578 GHRPTD 583
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C;Accession: T15030
R;Lindler, L.B.; Plano, G.V.; Burland, V.; Mayhew, G.F.; Blattner, F.R.
Infect. Immun. 66, 5731-5742, 1998
A;Title: Complete DNA Sequence and detailed analysis of the Yersinia pestis KIM5 plasmid
A;Reference number: Z18268; MUID:99043898; PMID:9826348
A;Accession: T15030
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A;Residues: Jreliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A;Cross-references: UNIPROT:Q92GX0; EMBL:AF074611; NID:g3883003; PID:g3883113; PIDN:AAC8
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A,Gene: Y1115
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-424-940A-1 Title: Perfect score: Sequence:

1 GHRPLDK 7

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	•	Description	P02677 canis famil	P02675 homo sapien	_		Q8elg4 streptococc		Q92xy9 rhizobium m	Q7mtw3 porphyromon	-	Q8sbaO oryza sativ	Q7xc70 oryza sativ	Q82d89 streptomyce	Q94e87 oryza sativ			Q8nh21 homo sapien			-		Q8k0e8 mus musculu		- '	Q6p3r6 homo sapien	_	Q46583 desulfovibr	Q6zq09 mus musculu	Q6p4s6 mus musculu	Q6ch64 yarrowia li	Q9y2k2 homo sapien	Q8r9g7 thermoanaer
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Kerst A.F.J.A., Lord S.T.;
"Abnormal fibrinogens IJmuiden (B beta Arg14---Cys) and Nijmegen (B beta Arg44---Cys) form disulfide-linked fibrinogen-albumin
                                                                         Yoshida N., Wada H., Morita K., Hirata H., Matsuda M., Yamazumi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT CONGENITAL AFIBRINOGENEMIA CYS-196.
MEDLINE=21361164; PubMed=11468164; DOI=10.1182/blood.V98.3.661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                             "A new congenital abnormal fibrinogen Ise characterized by the replacement of B beta glycine-15 by cysteine.";
Blood 77:1958-1963(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 41; DB 1; Length 491; 100.0%; Pred. No. 8.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANTS CONGENITAL AFIBRINOGENEMIA ARG-383 AND ASP-430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 afibrinogenemia by impairing fibrinogen secretion.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 89:3478-3482(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT NEW YORK-1 39-GLY--LEU-102 DEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANTS GLU-2; LEU-265 AND LYS-478.

    Biol. Chem. 260:4390-4396(1985).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clin. Invest. 90:238-244(1992).
                                        TEDLINE=91208409; PubMed=2018836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genet. 22:231-238(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genet. 23:373-373(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blood 95:1336-1341(2000).
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                                                                                                                                                                                                                                                                                        VARIANT NAPLES THR-98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GHRPLDK 7
VARIANT ISE ARG-45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human genes."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 Ala-->Thr."
J. Clin. Invest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complexes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lander E.S.;
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REQUENCE FROM N.A.

REQUENCE FROM N.A.

REQUENCE FROM N.A.

RADELINES-20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Cellniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Cellniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Holt R.A., Evans C.A., Galle R.F., Bardon R.C., Rogers Y.H., Elazej R.G., Champe M., Feffer B.D., R. Bardon R.C., Rogers Y.H., Elazej R.G., Champe M., Feffer B.D., R. Man K.H., Doyle C., Bardwin A., An H.J., Andrews-Flannkoch C., Baldwin D., Ballew R.M., Bans D.A., Barman B.P., Bhandari D., Bessley E.M., Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Burkis K.C., Busam D.A., Bulch K., Cadreu E., Center A., Chandra I., Burkis K.C., Busam D.A., Bulch K., Cadreu E., Center A., Chandra I., Burkis K.C., Busam D.A., Bulch K., Cadreu E., Center A., Chandra I., Burkis K.C., Busam D.A., Bulch K., Cadreu E., Center A., Chandra I., Bretz J. B., Davins B.D., Dewlin B., Burkis R., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dedon K., Deng Z., Mays A.D., Dew I., Dietz S.M., Ack Pablos B., Delcher A., Bowlend T.G., Gelbart W.M., Glasser K., Andreis N.L., Harvey D., Hemman T.G., Hernandez J.R., Houck J., Houston D., Markis N., Mays M., Hemman T.G., Hernandez J.R., Houck J., Houston D., Markis N., Mays M., Murphy B., Murphy D., Markis J., Mosherson D., Andrei B.E., Kodira C.D., Kraft C., Kravitz S., Rulp D., Lai Z., Leiteky A.A., Lid J., Marky D.M., Nelson D.L., Mount S.M., Moy M., Murphy B., Murphy L., Murzh D.M., Nelson D.L., Rollon K.A., Nixon R., Nusskern D.R., Palazzolo M., Pittman G.S., Pan S., Poll acher E., Spradling A.C., Stender E., Spradling A.C., Turner R., Venter E., Wang R., Santh T., Spier E., Spradling A.C., Turner R., Venter E., Wang A., Smith H.O., Rang K.H., Zhong F.M., Zhong W., Zhong W., Zhong W., Zhong W., Stubser M., Smith H.O., Rangerman D.A., Weissenbach G., Zhong W., Zhon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.; "The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Peieffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Frinishing a whole-genome shotgun: Release 3 of the Drosophila
                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                  Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22426065; PubMed=12537568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22426070; PubMed=12537573;
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                                                                                                                                         ORFNames=CG31013;
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OrderedLocusNames=gbs0427;
Streptococcus agalactiae (serotype III).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein gbs0427.
    Score 36; DB 2
Pred. No. 10;
0; Mismatches
                                                                                                                                                                                                                                   Transcriptional regulator, Fur family.
                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
  Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative (
                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                OrderedLocusNames=SAG0391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01475; FUR; 1.
ProDom; PD002003; FUR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                       18 GHRPADK 24
                                                          1 GHRPLDK 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome. SEQUENCE 159 AA;
                                                                                                                                                                                                                                                                                                      NCBI_TaxID=216466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=216495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGR; SAG0391; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GHRPLD 6
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01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                            Q8E1G4
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08E6Y1
1D 08E6F
DT 01-M
DT 01-M
DT 01-M
DE HYPOM
DE HYPOM
DC STREE
OC STREE
OX NCBI
RP SEQU
                                                                                                                               RESULT 5
                                                                                                                                               Q8E1G4
                                                                                                                                                                           FlyBase; FBgn0051015; PH4-alpha-PV.

FlyBase; FBgn0051015; PH4-alpha-PV.

GO; GO:0016706; Froxidoreductase activity, acting on paired d. . .; IEA.

GO; GO:0019538; P:protein metabolism; IEA.

InterPro; IPR005123; 20G-FeII Oxy.

InterPro; IPR006620; Pro 4 hyd alph.

Ffam; PP03171; 20G-FeII Oxy;

SMARI; SM00702; P446; 1.

SEQUENCE 404 AA; 46606 MW; 09330C64B0769F0R CPARA.
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Edvardsen R.B., Flat M., Tewari R., Jensen M.F., Seo H.C., Lehrach H., Reinhardt R., Chourrout D.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AF465689; AAM73994.1;

EMBL; AF465689; AAM73994.1;

GO; GO:0005525; F:GTP binding; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

GO; GO:0007198; P:microtubule-based movement; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                         MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Myxine glutinosa (Atlantic hagfish).
Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniformes;
                                                                                                                                            Lewis S.E.;
"Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.2%; Score 37; DB 2; Length 404; 85.7%; Pred. No. 48; 1; Mismatches 0; Indels
                                                                                                                                                                                                                              FlyBase;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                     FlyBase;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
EMBL; AE003774; AAF57073.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6375 MW; 0122F7B17D9D4B93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 22, Created)
(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002)
                                                                                                                                                                                    Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 AA.
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InterPro; IPR003008; Tubulin FtsZ.
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Myxinidae; Myxininae; Myxine
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 85.7°,
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alpha-tubulin 2 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00091; Tubulin; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                        systematic review.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GHRPLEK 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CHRPLDK 7
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58
58 AA;
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01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=TUBA2;
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SEQUENCE
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SEQUENCE FROM N.A.
STRAIN=2603 V/R / Serctype V;
MEDLINE=2222988; PubMed=1220547; DOI=10.1073/pnas.182380799;
Tettelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S.N., Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D., Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C., DeBOY R.T., Durkin A.S., Xolonay J.F., Madupu R., Lewis M.R., Radune D., Fedorova N.B., Scanlan D., Khouri H.M., Mulligan S., Carty H.A., Cilne R.T., Van Aken S.E., Gill J., Scarselli M., Mora M., Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D., Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA
InterPro; IPR002481; FUR.
InterPro; IPR009058; Wing hlx DNA bnd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence and comparative genomic analysis of an emerging human pathogen, serotype V Streptococcus agalactiae."; Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
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2; Length 58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus agalactiae (serotype V).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159 AA; 18584 MW; 31FBA715A358C127 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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us-09-424-940a-1.rup

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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
175 GHRPLD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CHRPLDK 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 GHRPTDK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 22-53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGR; PG1818; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-4.
                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FIBB BOVIN
P02676;
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                                                                                                                             Q7MTW3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FIBB BOVIN
                                                                             RESULT 8
                                                                                                     27MTW3
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MEDLINE=21396509; PubMed=11481432; DOI=10.1073/pnas.161294798;
MEDLINE=21396509; PubMed=11481432; DOI=10.1073/pnas.161294798;
Barnett M.J., Pisher R.F., Jones T., Komp C., Abola A.P.,
Barloy-Hubler P., Bowser L., Capela D., Galibert F., Gouzy J.,
Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
"Nucleotide sequence and predicted functions of the entire
                  MEDLINE-22242508; PubMed-12354221;
Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                  "Genome sequence of Streptococcus agalactiae, a pathogen causing invasive meonatal disease.";
MOI. Microbiol. 45:1499-1513 (2002).

EMBL; AL766845; CAD46071.1; -...

EMBL; AL766845; Piranscription factor activity; IEA.

GO; GO:0003700; Piranscription of transcription, DNA-dependent; IEA.

InterPro; IPR002481; FUR.

InterPro; IPR0020958; Wing_hlx_DNA_bnd.

Probom; PP004203; FUR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sinorhizobium meliloti psymA megaplasmid.";

Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).

-!- SIMILARITY: Contains 1 HTH tetR-type DNA-binding domain.

EMBL, AE007296; AAK65757.1; --

FRI, CG5399; CS5399.

GO; GO:0003700; F:transcription factor activity; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR009057; Homeodomain_like.

PRO0440; TetR.N; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.8%; Score 36; DB 2; Length 201; 100.0%; Pred. No. 37; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.8%; Score 36; DB 2; Length 159; 100.0%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome, Hypothetical protein.
SEQUENCE 159 Aa; 18584 MW; 31FBA715A358C127 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcription regulation. SEQUENCE 201 AA; 21500 MW; 447E9E9BF63EF551 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhizobium meliloti (Sinorhizobium meliloti).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 100.0%; Pred. No. 29, 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Putative transcriptional regulator. ORFNames=SMa2008;
STRAIN=NEM316 / Serotype III;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 GHRPLD 12
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                                                                                                Kunst F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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092XX9
092XX9
092XX
AC
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GHRPLD 6

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DOI=10.1128/JB.185.18.5591-5601.2003;
Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
Bisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
Dewhirst F.E., Fraser C.M.;
Complete genome sequence of the oral pathogenic bacterium
Orphyromonas gingivalis strain W83.";
J. Bacteriol. 185:5591-5601(2003).

EMBL, AE017,78; AAQ66816.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurús (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blomback B., Doolittle R.F.; "The N-terminal end of bovine fibrinopeptide B."; acids at the N-terminal end of bovine fibrinopeptide B."; Acta Chem. Scand. 17:1816-1819(1963).
                                                                                                                                                                      Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.8%; Score 36; DB 2; Length 238;
85.7%; Pred. No. 45;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1996 (Rel. 33, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Fibrinogen beta chain precursor [Contains: Fibrinopeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=79164394; PubMed=434821;
Martinelli R.A., Inglis A.S., Rubira M.R., Hageman T.C.,
Hurrell J.G.R., Leach S.J., Scheraga H.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome, Hypothetical protein.
SEQUENCE 238 AA; 26945 MW; DCA6C728CE6C8448 CRC64;
                                            01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
OrderedLocusNames=PG1818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 5-21.
Sioquist J., Blomback B., Wallen P.;
Sioquist J., Blomback B., Wallen P.;
"Amino acid sequence of bovine fibrinopeptides.";
Ark. Kemi 16:425-436(1960).
238 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 468 AA.
PRT;
                                                                                                                                                                                                                            Porphyromonadaceae; Porphyromonas.
                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22829867; PubMed=12949112;
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RESULT 10

28SBA0

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                                                                                                                              fibrinogen.";
Proc. Natl. Acad. Sci. U.S.A. 78:1466-1470(1981).
-!- FUNCTION: Fibrinogen has a double function: yielding monomers that
polymerize into fibrin and acting as a cofactor in platelet
                                                             SEQUENCE OF 44-468 FROM N.A.
MEDLINE-81199473; PubMed=6262803;
Chung D.W., Rixon M.W., McGillivray R.T.A., Davie E.W.;
"Characterization of a cDNA clone coding for the beta chain of bovine
                                                                                                                                                                                             SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains (alpha, beta and gamma), linked to each other by disulfide bonds. PTM: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopetides A and B from alpha and beta chains and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot. The soft clot is converted into the hard clot by factor XIIIA which catalyzes the epsilon-(gamma-glutamyl)lysine cross-linking between gamma chains (stronger) and between alpha chains (weaker) of different
 'Amino acid sequences of portions of the alpha and beta chains of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interchain (with alpha).
Interchain (with alpha).
Interchain (with alpha).
Interchain (with gamma).
Interchain (with gamma).
Interchain (with gamma).
By similarity.
By similarity.
By similarity.
N-linked (GlcNAc...) (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3D-structure, Blood coaqulation; Direct protein sequencing; Glycoprotein; Plasma; Platelet; Pyrrolidone carboxylic acid; Sulfation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cleavage (by thrombin; release fibrinopeptide B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fibrinopeptide B.
Fibrinogen beta chain.
Pyrrolidone carboxylic acid.
Sulfotyrosine.
                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Contains 1 fibrinogen C-terminal domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53340 MW; 2DED42F443AA4B37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00186; FBG; 1.
PROSITE; PS00514; FIBRIN AG C DOMAIN; 1.
                                Arch, Biochem. Biophys. 192:27-32(1979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDB; 1DEQ; X-ray; B/E/O/R=61468.
PDB; 1JY2; X-ray; O/R=61-116.
BDB; 1JY3; X-ray; O/R=61-116.
INCEPPC; IPRO02181; Fibringen_C.
Pfam; PF00147; Fibringen_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; V00110; CAA23444.1; -.
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468
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               fibrinogen."
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DISULFID
DISULFID
CARBOHYD
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DISULFID
DISULFID
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                 povine
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PRELIMINARY;
32 GHRPLD 37
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                     chromosome 10
                                                                   Q7XC70
                                       RESULT 11
                                                        07XC70
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                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                               87.8%; Score 36; DB 1; Length 468; 85.7%; Pred. No. 90;
                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                             Best Local Similarity
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22 GHRPYDK 28

1 GHRPLDK 7

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Matches

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Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N., Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsitrin T., Riggs F., Hsiao J., Zismann V., Blunt S., Pai G., VanAken S.E., Utterback T.R., Feldblyum T.V., Kalb E., Quackenbush J., Salzberg S.L., White O., Fraser C.M.; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                       Oryza sativa (Rice).
Mkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "In-depth view of structure, activity, and evolution of rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 471;
91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.,
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AR017119; AAPS55004.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                               Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AC079874; AAL79787.1; -.
Gramene, Q88BA0; -.
GO; GO:0008415; F:acyltransferase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR00123; Acyltransferase.
Ffam; PF01553; Acyltransferase; 1.
SWART; SM00563; P18C; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50200 MW; 75D92E78D51937DD CRC64;
                                                01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypotheitcal protein OSJNBa0042H09.17.
Name-OSJNBa0042H09.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87.8%; Scor.
100.0%; Pred. No. ...
 471 AA
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                                01-JUN-2002 (TrEMBLrel. 21, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 300:1566-1569(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
ORFNames=OSJNBa0042H09.17;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            al protein.
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                                                                                                                                                                                           NCBI_TaxID=4530;
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QBSBAO
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PubMed=1247438; DOI=10.1038/nature01184;
A Saski T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y., Saski T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Kanamori H., Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H., Antokawa S., Machawa K., Arita K., Hamada M., Harada C., Hijiahida S., Honda M., Ichikawa Y., Idonuma A., Iijiam M., Iteda M., Ichikawa Y., Itcho Y., Machai Y., Matagasaki H., Nakasina T., Mixuno H., Mixubayashi T., Mukai Y., Nagasaki H., Nakashima M., Nakama Y., Ono N., Saji S., Sakai, K. Shibata M., Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K., A Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K., Zhong H., Iwama H., Edo T., Itch H., Hahn J.H., Kim H.I., Eun M.Y., A Yano M., Jiang J., Gojobori T.;
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nyakatura G., Fartmann B., Dauner D., Sterr W., Holland R.,
Weichselgartner M., Mewes H.W., Lemcke K., Mayer K.F.X., Quetier F.,
Salanoubat M.;
                                                                                                                                                                             Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaea; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The genome sequence and structure of rice chromosome 1.";
Nature 420:312-316(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 735;
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Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
-!- SIMILARITY: Belongs to the ABC transporter family.
EMBL; AL138658; CAB75931.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
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SEQUENCE 735 AA; 79897 MW; 540392FCBF125EF6 CRC64;
                                                                 Last sequence update)
Last annotation update)
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Last annotation update)
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100.0%; Pred. No. 1.4e+02;
iive 0; Mismatches 0;
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                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created) 01-OCT-2000 (TrEMBLrel. 15, Last seq 01-OCT-2003 (TrEMBLrel. 25, Last ann Multi resistance protein homolog.
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Interpro, IPR008940; Prenyl_trans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AP003199; BAB61147.1; -.
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                                                                                                                    B1045D11.13 protein.
Name=B1045D11.13;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                  NCBI_TaxID=39947;
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Matches
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        ACCOCCOSON TO THE SECOND THE SECO
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Sakaki Y., Hattori M., Omura S.;
                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=MA-4680;
MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
metabolites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                     87.8%; Score 36; DB 2; Length 471; 100.0%; Pred. No. 91; o; Indels ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.4e+02;
.ive 0; Mismatches 0; Indels
GO; GO:0008415; F:acyltransferase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR002123; Acyltransferase.
Pfam; PF01553; Acyltransferase; 1.
Hypothetical protein.
SEQUENCE 471 AA; 50200 MW; 75D92E78D51937DD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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MEDLINE=22608306; PubMed=12692562;
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                                                                                                                                                                                                                                                                 6; Conservative
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GHRPLD 349
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Best Local Similarity
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SEQUENCE 732 AA;
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01-JUN-2003
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RESULT 13 Q94E87 ID Q94E8

Matches

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Indels

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R GO; GO:0016021; C:integral to membrane; IEA.

R GO; GO:0016021; C:integral to membrane; IEA.

R GO; GO:0016021; C:integral to membrane; IEA.

R GO; GO:0001662; F:ATP binding; IEA.

R GO; GO:0001662; F:nucleotide binding; IEA.

R GO; GO:0001662; F:nucleotide binding; IEA.

R GO; GO:0001661; P:nucleotide binding; IEA.

R GO; GO:0001661; P:nucleotide binding; IEA.

R GO; GO:0001661; P:nucleotide binding; IEA.

R InterPro; IPR001303; AAA ATPase.

R InterPro; IPR001303; AAA ATPase.

R InterPro; IPR001319; ABC Transporter.

R Ffam; PF00005; ABC Transporter; 2.

R Frobom; PF00005; ABC Transporter; 2.

R ROSITE; PS50929; ABC TRANSPORTER 1; 1.

R ROSITE; PS50893; ABC TRANSPORTER 1; 1.

R ROSITE; PS50893; ABC TRANSPORTER 1; 1.

R ROSITE; PS50893; ABC TRANSPORTER 2; 2.
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MEDLINE-22608657; PubMed=12704232; DOI=10.1073/pnas.0931379100;
Seshadri R., Paulsen I.T., Eisen J.A., Read T.D., Nelson K.E.,
Nelson W.C., Ward N.L., Tettelin H., Davidsen T.M., Beanan M.J.,
DBBOY R.T., Daugherty S.C., Brinkac L.M., Madupu R., Dodson R.J.,
Khouri H.M., Lee K.H., Cartry H.A., Scanlan D., Heinzen R.A.,
Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F.;
"Complete genome sequence of the Q-fever pathogen, Coxiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.8%; Score 36; DB 2; Length 1490;
100.0%; Pred. No. 3e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1490 AA; 166455 MW; 237FCE03A3B4DA0F CRC64;
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InterPro; IPR003509; UPF0102.
Pfam; PF02021; UPF0102; 1.
COMPLETE ; TIGR0052; UPF0102; 1.
COMPLETE proteome; Hypothetical protein.
SEQUENCE 120 AA; 14231 MW; A41A98C6B80DAE33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 100:5455-5460(2003).
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29-MAR-2004 (Rel. 43, Last sequence update)
20-ULJ-2004 (Rel. 44, Last annotation update)
Hypothetical UPF0102 protein CBU1742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OrderedLocusNames=CBU1742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coxiellaceae; Coxiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1226 GHRPLD 1231
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Q83AYS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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YH42_COXBU
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OR NO DE RESERVA DE RE
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WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&
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                           ö
                                                                                                                                                                                                                                                                                                                                 Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
"Genome-wide discovery and analysis of human seven transmembrane helix
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                      Submitted (ULL-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Putative odorant receptor.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
-!- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium
                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                           ö
 1; Length 120;
                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Multigene family; Olfaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (Potential).
Cytoplasmic (Potential).
2 (Potential).
3 (Potential).
Cytoplasmic (Potential).
4 (Potential).
Extracellular (Potential).
5 (Potential).
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6 (Potential).
Extracellular (Potential).
7 (Potential).
Cytoplasmic (Potential).
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70E99D068AB2DD59 CRC64;
                           ö
                                                                                                                                                                            10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
85.4%; Score 35; DB:
100.0%; Pred. No. 35;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew; HGNC:14825; OR4F5.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR000725; Olfact_receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB065592; BAC05820.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00237; GPCRRHODOPSN. PRINTS; PR00245; OLFACTORYR.
Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00001; 7tm 1; 1.
                                                                                                                                                                                                                       Olfactory receptor 4F5.
                                                                                                                                                                                                                                                   Homo sapiens (Human)
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305 AA;
                                                                               88 HRPLDK 93
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                    2 HRPLDK 7
                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                              receptor genes."
Submitted (JUL-2)
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                                                                                                                                                                                                                                      Name=OR4F5;
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O4F5_HUMAN
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A Straubberg R.L., Feingold E.A., Grouse L.H., Darge J.G.,
Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
R. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heideh F.,
Brantenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Robark S.A., McEwan P.J., McKernan K.J., Malke J.A., Gunzartne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Antingki M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                       Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Fibrinogen beta chain precursor [Contains: Fibrinopeptide
              85.4%; Score 35; DB 1; Length 305; 100.0%; Pred. No. 93; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.4%; Score 35; DB 2; Length 390
85.7%; Pred. No. 1.2e+02;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC035583; AAH35583.2; -.
Hypothetical protein.
SEQUENCE 390 AA; 42414 MW; 466BF7F6AEDA051C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                    01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                   390 AA.
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                                                     6; Conservative
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Matches 6; Conservative
                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                220 HRPLDK 225
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              Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                            2 HRPLDK 7
                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606
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FIBB_CHICK
ID FIBB_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S., Tsutsumi S., Aburatani H., Asai K., Akiyama Y.; "Genome-wide discovery and analysis of human seven transmembrane helix
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Putative odorant receptor.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DATABASE: NAME-Human Olfactory Receptor Data Exploratorium
                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                       ;
0
              DB 1; Length 305; 93;
                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genew; HGNC:15381; ORAFI7.
InterPro; IPR000276; GPCR Rhodpsn.
InterPro; IPR000275; GPCR Rhodpsn.
Pression; PR00017; Trm 1; 1.
PRINTS; PR00237; GPCRHODOPSN.
PRINTS; PR00237; GPROTEIN RECEP_F1_1; 1.
PROSITE; PS00237; GPROTEIN RECEP_F1_2; 1.
PROSITE; PS00262; GPROTEIN RECEP_F1_2; 1.
G-protein coupled receptor; Multigene family; Olfaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (JUL-2001) to the EMBL/GenBank/DDBJ databases
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1 (Potential).
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Extracellular (Potential).
3 (Potential).
Cytoplasmic (Potential).
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Extracellular (Potential)
5 (Potential).
Cytoplasmic (Potential).
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Extracellular (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 (Potential).
Cytoplasmic (Potential).
                                                                                                                                                                                                                                                               10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Alfactory receptor 4F17.
Name-OR4F17; Synonyms-OR4F19;
85.4%; Sco...
100.0%; Pred. No. >-,
                                                                                                                                                                                                                                 305 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity
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                                                   6; Conservative
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220 HRPLDK 225
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90
305 AA;
            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                        2 HRPLDK 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor genes.";
Submitted (JUL-20
                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                 04FH HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Suwa M.,
Tsutsumi
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DISULFID
SEQUENCE
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TRANSMEM
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWIS
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                                                   Matches
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FIBB RAT
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                                                                                                                                                                                                                                 monomers that
                                                                                                                                                                                                                                                            SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains (alpha, beta and gamma), linked to each other by disulface bonds. PTM: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopeptides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot. The soft clot is converted into the hard clot by factor XIIA which catalyzes the epsilon-(gamma-glutamyl)lysine cross-linking between gamma chains (stronger) and between alpha chains (weaker) of different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (By similarity).
(By similarity).
(By similarity).
(By similarity).
(By similarity).
                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF 1-13 AND 18-39.
MEDLINE-91182745; PubMed=2009266;
Weisebach L., Oddoux C., Procyk R., Grieninger G.,
"The beta chain of chicken fibrinogen contains an atypical thrombin
                                                                                                                                                                                           cleavage site.";
Biochemistry 30:3290-3294(1991).
-!- FUNCTION: Fibrinogen has a double function: yielding monomes
polymerize into fibrin and acting as a cofactor in platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . .) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fibrinopeptide B.
Fibrinogen beta chain.
Fibrinogen beta chain.
Cleavage (by thrombin; release fibrinopeptide B).
Interchain (with alpha) (By simil Interchain (with alpha) (By simil Interchain (with gamma) (By simil By similarity.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE, PS00514; FTBRIN AG C DOMAIN; 1.
3D-structure; Blood coagulation; Direct protein sequencing; Glycoprotein; Plasma; Platelet; Sulfation.
NON TER
1 17 Fibrinopeptide B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 463,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: Contains 1 fibrinogen C-terminal domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35; DB 1;
Pred. No. 1.4e+0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDB; 1E13; X-ray; B/E=1-463.
PDB; 1MlJ; X-ray; B/E=1-463.
InterPro; 1PR002181; Fibrinogen_C.
Pfam; PF00147; Fibrinogen_C; 1.
SWART; SM00186; FBG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52678 MW;
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              Gallus gallus (Chicken)
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201
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                                                                                     NCBI_TaxID=9031;
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    liver regeneration.";
Exp. Cell Res. 169:47-56(1987).
-1-FUNCTION: Fibrinogen has a double function: yielding monomers that
polymerize into fibrin and acting as a cofactor in platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eggregation.

--- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains (alpha, beta and gamma), linked to each other by disulfide bonds.

--- FTM: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinogeptides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot.

--- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 183-479 FROM N.A.
MEDLINE=89378771; PubMed=2673932; DOI=10.1016/0378-1119(89)90100-5;
Eastman E.M., Gilula N.B.;
"Cloning and characterization of a cDNA for the B beta chain of rat
fibrinogen: evolutionary conservation of translated and 3'-
untranslated sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Wistar; TISSUE-Liver;
MEDLINE=87134033; PubMed=3817019;
SObczak J., Lotti, A.-M., Taroux P., Duguet M.;
"Molecular cloning of mRNA sequences transiently induced during rat
                                                                                                                                                                                                                                                                      STRAIN=Sprague-Dawley, TISSUB-Liver, MEDLINE-55143386; PubMed=7841303; Courtney M.A., Bunce L.A., Neroni L.A., Simpson-Haidaris P.J.; Courtney M.A., Edge complete coding sequence of rat fibringen B beta chain cDNA: interspecies conservation of fibrin beta 15-42 primary
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-26 FROM N.A.
MEDLINE=84194000; PubMed=6232608;
Fowlkes D.M., Mullis N.T., Comeau C.M., Crabtree G.R.;
Forential basis for regulation of the coordinately expressed fibrinogen genes: homology in the 5' flanking regions.";
Proc. Natl. Acad. Sci. U.S.A. 81:2313-2316(1984).
                                                            01-OCT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Fibrinogen beta chain precursor (Contains: Fibrinopeptide B)
479 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blomback B., Blomback M., Grondahl N.J.; "Studies on fibrinopeptides from mammals."; Acta Chem. Scand. 19:1789-1791(1965).
                                                                                                                                                                                                                                                                                                                                                                          structure.";
Blood Coagul. Pibrinolysis 5:487-496(1994).
                                         01-JAN-1990 (Rel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 425-479 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, U05675; AAA64866.1; -.
EMBL, MA7220; AAA11160.1; -.
EMBL; K01336; AAA98625.1; -.
EMBL; M35602; AAA41159.1; -.
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene 79:151-158(1989).
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                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                             Name=Fqb;
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HRPLDK 24 HRPLDK 7

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Gaps

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Indels

1.4e+02;

100.0%; Prec. ...

Conservative

Local Similarity

Best Locy Matches

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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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STRAINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
M. Klausner R.D., Collins F.S., Wagner L., Shemmen C.W., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley D.M., Sodrcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzry D.M., Sacria A.M., Gay L.J., Hulyk S.W.,
Willalon D.K., Muzry D.M., Shevchenko Y., Bouffard G.G.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
PIR; I67595; I67595.
HSSP; P02675; IFZE.
RGD; F9b.
TinterPro; IPR002181; Fibrinogen C.
Pfam; PF00147; Fibrinogen C; 1.
SMART; SM00186; P8G; 1.
BROSTIE; PS00514; FIBRIN AG C DOMAIN; 1.
Blood coagulation; Direct protein sequencing; Glycoprotein; Plasma;
                                                                                                                                                                                                                                                                                                                                            304 By similarity.
258 By similarity.
425 By similarity.
382 N-linked (GlCNAc. . .) (Potential).
30 LSI -> ILS (in Ref. 3).
439 L -> Q (in Ref. 5).
441 S -> A (in Ref. 5).
457 S -> A (in Ref. 5).
475 V -> F (in Ref. 5).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Interchain (with alpha chain)
                                                                                                                                                                                                                                                                                     similarity).
Interchain (with gamma chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 85.4%; Score 35; DB 1; Length 479; Similarity 71.4%; Pred. No. 1.5e+02; 5; Conservative 2; Mismatches 0; Indels
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                       Fibrinogen beta chain.
                                                                                                                                                                                                                                                                                                                                 similarity).
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479 AA;
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SIGNAL
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Xu C.S., Li W.Q., Li Y.C., Chang C.F., Chai L.Q., Yuan J.Y.,
Yang K.J., Yan H.M., Zhao L.F., Ma H., Wang L., Wang S.F., Han H.P.,
Wang G.P., Shi J.B., Rahman S., Wang Q.N., Zhang J.B.,
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
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0
                                                   Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (UUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC031715; AR431715.1; -.
RSS; PO2675; 1FZB.
RGG; GO3005615; C:extracellular space; TAS.
RG; GO; GO005615; C:extracellular space; TAS.
RICEPRO; IRRO0181; Fibrinogen C.
R Ffan; PR00147; Fibrinogen C; 1.
R SMART; SM00186; FBG; 1.
R SMART; SM00186; FBG; 1.
R SCOUENCE 481 AA; 54752 MW; 9902830CF708A155 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 85.4%; Score 35; DB 2; Length 481; Best Local Similarity 71.4%; Pred. No. 1.5e+02; Matches 5; Conservative 2; Mismatches 0; Indels
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503 AA; 56612 MW; 02B6A1E05E7B5C12 CRC64;
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01-077-2003 (TrEMBLrel. 25, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Ac1-581 (Ab1-216) (Ab1-181).
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71.4%; Pred. No. 1.6e+02;
ive 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      503 AA.
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EMBL, AY325153; AAP92554.1; -...
EMBL, AY325147; AAP92548.1; -...
HSSP, PO2675; 1FZC.
InterPro; IPR002181; Fibrinogen_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam, PF00147, Fibrinogen_C; 1. SWART, SM00186; FBG; 1. PROSITE, PS00514; FIBRIN AG C D
SEQUENCE FROM N.A. STRAIN=FVB/N; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GHRPLDK 7
||||:||:
35 GHRPVDR 41
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32 GHRPVDR 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [2]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
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sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse
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Q641L5
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                                                                                                                                                                                                                                                                                                                                                                             RCESUDE-Mammary gland;

RC TISSUE-Mammary gland;

RA OTA T., Sulviki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,

RA OTA T., Sulviki Y., Satol H., Nagai K., Kimura K., Makita H.,

RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

RA Amamoto J., Saitok K., Rawai Y., Isono Y., Nakamura Y., Nagahari K.,

RA Murakani K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratoria A.,

RA Abe K., Kamihara K., Kateuta N., Sato K., Tanikawa M., Yamazaki M.,

RA Abe K., Ishibashi T., Yamashita H., Murakawa M., Yamazaki M.,

RA Abe K., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,

RA Anai H., Kimata M., Watanabe S., Yosida M., Hotuta T., Kusano J.,

RA Anai H., Matanabe T., Hara H., Tanase T., Nomura Y.,

RA Musashino K., Yuuki H., Oshima A., Satoki N., Arita M., Imose N.,

Musashino K., Yuuki H., Oshima A., Satoki N., Sano S.,

Nochikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,

Nochikawa Y., Matsunawa H., Takina M., Incawi S.,

RA Makagawa S., Sonoh A., Mizoguchi H., Goto Y., Shiniazu F., Wakebe H.,

RA Hishigaki H., Watanabe K., Kumagai A., Itakura S., Pukuzumi Y.,

Ramazaki M., Watanabe K., Kumagai A., Itakura S., Pukuzumi Y.,

Ramazaki M., Watanabe K., Kumagai A., Itakura S., Pukuzumi Y.,

Ramazaki M., Watanabe K., Kumagai A., Itakura S., Pukuzumi Y.,

Ramazaki M., Watanabe K., Kumagai A., Itakura S., Pukuzumi Y.,

Ramazaki M., Watanabe Y., Moguchi S., Itoh T., Shigeta K., Senba T.,

Rabimori K., Rawakami T., Moguchi S., Itoh T., Shigeta K., Senba T.,

Matsumura K., Bakaila Y., Mata H., Watanabe M., Komatsu T.,

Matsumura K., Nakajima Y., Mataura Y., Okamoto S.,

Matsumura K., Nakajima Y., Mataura Y., Ohmori Y., Yamashita R.,

Matsumura K., Nagase T., Nomura N., Kiuchi H., Manuno S.,

Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,

Ramazaki W., Wakamura Y., Ohara O., Isogai T., Sakai M.,

Ramazaki M., Watanatering and characterization of 21,243 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Petroziello J., Carter P.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AK022332; BAB14006.1; -.
EMBL; AYS98333; AAT06749.1; -.
SEQUENCE 505 AA; 54782 MW; 43BADEB48CODFBE7 CRC64;
                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical PL012240 (L19).
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Last annotation update)
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O6P3R6;
O5-UUL-2004 (TrEMBLrel. 27, C)
O5-UUL-2004 (TrEMBLrel. 27, Ls
O5-UUL-2004 (TrEMBLrel. 27, Ls
KIAA0999 protein.
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                                                                          PRELIMINARY;
                                                                                                                                                                                                                                       Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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                                                                          Q9HA50
                   RESULT 23
Q9HA50
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Q6P3R6
ID Q6P3R
AC Q6P3R
DT 05-JU
DT 05-JU
DT 05-JU
DE KIAA0
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MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Felingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B. Buetcw K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B. Buetcw K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A platchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,
Anilalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pubmed=12477932; DDI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Maruslina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; BC063887; AAH63887.1; -.
SEQUENCE 598 AA; 65097 MW; 58754EDC85E47598 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0641L5;
25-OCT-2004 (TrEMBLrel. 28, (
25-OCT-2004 (TrEMBLrel. 28, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA sequences.
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                               SEQUENCE FROM N.A.
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Name=BC033915;
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                                                                           NCBI_TaxID=9606;
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SMART; SM00304; HAMP; 1.
                                                                                                                                2 HRPLDK 7
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                                                                                                                                                                                                                                                                                        Name=mKIAA0999
                                                                                    Query Match
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Q6P4S6
                                                                                                                                                                                           RESULT 27
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Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Vrones S.J., Marra M.A.;
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Hildenborough;
MEDLINE-9643451; PubMed=8836438;
Deckers H.M., Voordouw G.;
"The dcr gene family of Desulfovibrio: implications from the sequence of dcrH and phylogenetic comparison with other mcp genes.";
Antonie Van Leeuwenhoek 70:21-29(1996).
PIR; H36943; H36943.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Hildenborough, MEDLINE=94117369; MEDLINE=94117369; PubMed=8288529; Deckers H.M., Voordouw G.; Indentification of a large family of genes for putative chemoreceptor proceins in an ordered library of the Desulfovibrio vulgaris
                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              Desulfovibrio vulgaris.
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
Desulfovibrionaceae; Desulfovibrio.
NCBI_TaxID=881;
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                                                                                                                                                                                                   85.4%; Score 35; DB 2; Length 643;
85.7%; Pred. No. 2e+02;
iive 0; Mismatches 1; Indels
                                                                                                                  SEQUENCE FROM N.A. STRAIN; STRAIN=C57BL/6; TISSUE=Brain; Director MGC Project; Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases. EMBL; EC082313; AAH82313.1; -.
                                                                                                                                                                             70222 MW; EE66AF7C3AC1310B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P02942; 1007.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0005506; F:iron ion binding; IEA.

GO; GO:0005344; F:oxygen transporter activity; IEA.

GO; GO:00064871; F:signal transducer activity; IEA.

GO; GO:0006935; P:chemotaxis; IEA.

GO; GO:000165; P:signal transduction; IEA.

GO; GO:0006810; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                     959 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR004089; Chmtaxis transd.
InterPro; IPR002063; Hemerythrin.
InterPro; IPR003660; His kin_HAMP.
Pfam; PP00672; HAMP; 1.
Pfam; PP01814; Hemerythrin; 1.
Pfam; PP00015; MCP8ignal; 1.
ProDom; PD006099; Hemerythrin; 1.
                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hildenborough genome.";
J. Bacteriol. 176:351-358(1994)
                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                         179 GHRPLSK 185
                                                                                                                                                                             643 AA;
                                                                                                                                                                                                                                                   1 GHRPLDK 7
                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                        Name=dcrH;
                                                                                                                                                                                                    Query Match
                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                     046583
                                                                                                                                                                                                                                                                                                           Matches
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PubMed=14621295;

PubMed=14621295;

Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S., Saga Y., Nagase T., Ohara O., Koga H.;

"Prediction of the coding sequences of mouse homologues of KIAA gene: III. the complete mucleotide sequences of 500 mouse KIAA-homologous convas identified by screening of terminal sequences of cDNA clones randomly sampled from size-fractionated libraries.";

EMBL; AKI29257; BRO98067.1; -.

InterPro; IPR000449; UBA.

InterPro; IPR000660; UBA.

PROSITE; PSS0030; UBA; 1.
                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA sequence BC033915.

Name=BC033915;

Name=BC033915;

Mas musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.4%; Score 35; DB 2; Length 1052;
85.7%; Pred. No. 3.48+02;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                     Length 959;
                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 1052 AA; 115918 MW; 6DESF456329E21A4 CRC64;
                                                                                                                        450550E840954D42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q6P486; Q66JZ5;
Q6-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                 85.4%; Score 35; DB 2; Le
100.0%; Pred. No. 3.1e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1052 AA.
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SMART; SM00283; MA; 1.
PROSITE; PS5011; CHEMOTAXIS_TRANSDUC_2; 1.
PROSITE; PS50885; HAMP; 1.
PROSITE; PS00550; HEMBEXTHRINS; UNKNOWN 1.
SEQUENCE 959 AA; 104728 MW; 450550E8409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MKIAA0999 protein (Fragment).
                                                                                                                                                                                                              Best Local Similarity 100. Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              588 GHRPLSK 594
                                                                                                                                                                                                                                                                                                                                                                513 HRPLDK 518
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Yarrowia lipolytica CLIB99
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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
HOPKINS R.F., Jordan H., Moore T., Max S.I., Kang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Bromstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A'Illalon D.K., Maxny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A'Illalon D.K., Maxny D.M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A'Dones S.J., Marra M.A.;
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                          Defector Model Project;

Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.

- 1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

R EMBL; BCG63268; AAH60568: 1; -

R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0004713; F:protein serine/threonine kinase activity; IEA.

R GO; GO:0004713; F:protein serine/threonine kinase activity; IEA.

R GO; GO:0004713; F:protein serine/threonine kinase activity; IEA.

R GO; GO:0006468; P:protein again activity; IEA.

R GO; GO:0006469; P:protein amino acid phosphorylation; IEA.

InterPro; IPR001099; Kinase.

R InterPro; IPR002290; Ser_thr_pkinase.

R InterPro; IPR002245; Tyr_pkinase.

R InterPro; IPR00445; UBA.

R InterPro; IPR00445; UBA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP-binding, Kinase, Serine/threonine-protein kinase, Transferase.
SEQUENCE 1311 AA; 145810 MW; CF111B8995BC3F2B CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to sp|P13433 Saccharomyces cerevisiae DNA-directed RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ub ...
4.3e+02;
1; Indels
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRANT=FVB/N; TISSUE=Salivary gland;
Director MGC Project;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00069; Pkinase; 1.

SMART; SM00209; Trc, 1.

SMART; SM00219; TyrKc; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN 1.

PROSITE; PS00108; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.4%; Score 35; DB 2;
85.7%; Pred. No. 4.3e+02
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-0CT-2004 (TrEMBLrel. 28, Created)
25-0CT-2004 (TrEMBLrel. 28, Last seq
25-0CT-2004 (TrEMBLrel. 28, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 85.,°,
Best Gonservative
                                                                                                                                                                                                                                  and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polymerase.
ORFNames=YALIOA12001g;
                                                                                                                                                                                                                                                                                                                                                                 Director MGC Project;
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                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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ID OGCH64-
DT 255
DT 255
DT 255
DE SI
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Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Goffard N., Frangeul L., Aigle M., Anthourad V., Babour A., Barbe V.,
Goffard N., Frangeul L., Aigle M., Anthourad V., Babour E.,
Barnay S., Blanchin S., Beckerich J.M., Beyne B., Eleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Boisrame A., Roszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Swennene D., Tekata F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Mincker P., Souciet J.L.;
"Genome evolution in yeasts.";

    -!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
of DNA into RNA using the four ribonucleoside triphosphates as
substrates (By similarity).

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   {RNA}(N).
-!- SIMILARITY: Belongs to the phage and mitochondrial RNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
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GO; GO: 0003899; F:DNA-directed RNA polymerase activity; IEA.
GO; GO: 0003899; F:DNA-directed RNA polymerase activity; IEA.
GO; GO: 0005350; F:DNA-directed RNA polymerase.
InterPro; IPR002092; RNA pol_phage.
PROMITE; PS00940; RNA POL_PHAGE 1; 1.
PROSITE; PS00489; RNA POL_PHAGE 2; 1.
DNA-directed RNA POLYMETASE; Transcription; Transferase.
SEQUENCE 1345 AA; I52077 MW; D2A7B91A9F970244 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.4%; Score 35; DB 2; Length 1345; 100.0%; Pred. No. 4.4e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1999 (TrEMBLrel. 12, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-WAR-2004 (TrEWBLrel. 26, Last annotation update)
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Name=KIAA0999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dest Match
Best Local Similarity 100.vv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 430:35-44 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1281 HRPLDK 1286
                                                       NCBI TaxID=284591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 HRPLDK 7
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                                                                                                                                                              STRAIN=CLIB99;
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                                                                                                                                                                                                 Genolevures
                                                                                                                            SEQUENCE
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hoved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                    HSSP; P3338; 1DLG.
HAWAP; MF 00111; -; 1.
InterPro; IPR005750; AcGlu Tran MurA.
InterPro; IPR01986; BESP Synth.
Pfam; PF00275; BESP Synthase; 1.
ProDom; P001867; EPSP synth; 1.
TIGRFMMs; TIGR01072; murA; 1.
Cell division; Cell wall; Complete protecome; Peptidoglycan synthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ueda K., Yamashita A., Ishikawa J., Shimada M., Watsuji T.,
Morimura K., Ikeda H., Hattori M., Beppu T.;
"Complete genome sequence of an uncultured bacterium Symbiobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 116 PEP (covalent) (By similarity) 417 AA; 45211 MW; 0A199EC2B104DC6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.9%; Score 34; DB 1; Length 417; 83.3%; Pred. No. 2.1e+02; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.9%; Score 34; DB 2; Length 424; 71.4%; Pred. No. 2.1e+02; Live 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proton donor (By similarity)
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EMBL; AP006840; BAD42285.1; -.
GO; GO:0016740; F:transferase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         424 AA; 45497 MW; 004C2B0B0C064DAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
UDP-N-acetylglucosamine enolpyruvyl transferase.
ORFNames=STH3304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           424 AA
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NCBI_TaxID=2734;
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InterPro; IPR001986; BPSP Bynth.
Pfam; PF00275; BPSP synthāse; 1.
ProDom; PD001867; BPSP synth; 1.
                                                                                                                                                                                                                                           EMBL; AE013119; AAM24846.1; -
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Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Conservative
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116
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121 GHRPVDQ 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 GHRPID 124
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ACT_SITE
BINDING
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Q7S2E9;
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ID Q7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                               Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirosawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XIII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.", DNA Res. 6:63-70(1999).

-- Ishilamirar: Belongs to the Ser/Thr protein kinase family. EMBL; AB021216; BAA76843.2; -- HSSP; P49137; 1NY3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- SIMILARITY: Belongs to the EPSP synthase family. MurA subfamily.
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28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
UDP-N-acety1glucosamine 1-carboxyvinyltransferase 2 (EC 2.5.1.7)
(Enoylpyruvate transferase 2) (UDP-N-acety1glucosamine enolpyruvyltransferase 2) (EPT 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pfam; PF00069; Pkinase; 1.
SMART; SM00200; S TKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE ST; 1.
PROSITE; PS00109; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
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-!- CATALYTIC ACTIVITY: Phosphoenolpyruvate + UDP-N-acetyl-D-
glucosamine = phosphate + UDP-N-acetyl-3-0-(1-carboxyvinyl)-D-
                                                                                                                                                                                                                                                                                                                                  GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:protein serine/threonine kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0016648; P:protein amino acid phosphorylation; IEA.
InterPro; IPR011009; Kinase like.
InterPro; IPR00219; Prot Kinase.
InterPro; IPR00229; Ser_thr_pkinase.
InterPro; IPR00249; Ser_thr_pkinase.
InterPro; IPR000449; UBA.
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85.7%; Pred. No. 4.5e+02;
iive 0; Mismatches 1; Indels
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Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1371 AA; 149525 MW; FOFBA385B8226158 CRC64;
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          MEDLINE=99246063; PubMed=10231032;
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Matches 6; Conservative
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InterPro; IPR000719; Prot kinase.
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Name=SPBP8B7.23;
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                                                                                                                                                                                                                                                                                                                      ATP-binding.
SEQUENCE 4
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094271
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BODEN CCELERAR BERRER BERR
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Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
Blking T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
A Qui D., Janakiev P., Pedersen D., Nelson M., Washburne M.,
Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
Korthe G.O., Jedd G., Mewes W., Staben C., Marcette E., Greenberg D.,
Roy A., Foley K., Naylor J., Mauceli E., Bielke C., Rudd S., Frishman D.,
Krystofova S., Rasmussen C., Mezenberg R.L., Perkins D.D., Kroken S.,
Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.,
Warten O., Plamann Sequence of the Filamentous Fungus Neurospora crassa.",
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PubMed=15001715; DOI=10.1126/science.1095781;
Dietrich F.S., Voegeli S., Brachat S., Lerch A., Gates K., Steiner S., Mohr C., Pohlmann R., Ludeli P., Choi S., Wing R.A., Flavier A., Gaffney T.D., Philippsen P.;
The Ashbya gossypii genome as a tool for mapping the ancient Saccharomyces cerevisiae genome.";
Science 304:304-307(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Eremothecium.
NCBI_TaxID=33169;
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GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:000648; P:protein amino acid phosphorylation; IEA.
InterPro; IPR011009; Kinase_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 0:0-0(2003).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                       Neurospora crassa.
Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.9%; Score 34; DB 2; Length 426; 71.4%; Pred. No. 2.1e+02; tive 2; Mismatches 0; Indels
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SEQUENCE 426 AA; 48541 MW; 8D93CB4C4625B926 CRC64;
Created)
Last sequence update)
Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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01-MAR-2004 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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97 GHQPLDR 103
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                                                                                             Predicted protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 34
Q751V1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGD;
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MACHILIMESTREAGES, TUDENTINDS/ANDLESSES, MEDILINESTREAGES, MEDILINESTREAGES, MEDILINESTREAGES, MEDILINESTREAGES, MEDILINESTREAGES, MEDILINESTREAGES, MEDILINESTREAGES, Basham D., Bowman S., Bacoks K., Brown D., Brown S., Chillingworth T., Churcher C., Connor R., Cronin A., Davis D., Hidalgo J., Hodgson G., A Collins M., Connor R., Hamlin N., Harris D., Hidalgo J., Hodgson G., Harnsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Ra James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Ra James K., Jones L., Saunders B., Gusis M., Rabbinowitsch E., Rutherford K., Rutter S., Saunders B., Stevens K., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., Rablor K., Taylor R.G., Tivey A., Walsh S., Warren T., Whitehead S., Relton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor R.G., Taylor R.G., Aert R., Robben J., Grymonprez B., A Woldward J., Volckaert G., Aert R., Robben J., Grymonprez B., A Weltjens I., Vanstreels E., Rieger M., Schafer M., Muller-Auer S., A Dohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., A Lucas M., Rochet M., Gaillardin C., More K., Hurte C., Moore X., Hurte S., M., Gerzon A., Thode G., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Shander B., Shakovski G.V., Ubsery D., Barrell B.G., Narre P.;

The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.9%; Score 34; DB 2; Length 440; 85.7%; Pred. No. 2.2e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=972h-; MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724; MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GeneDB SPombe; SPBPBB7.23; -. GO; GO:0000151; C:ubiquitin ligase complex; IEA. GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA. GO; GO:0008270; F:zinc ion binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                  440 AA; 50173 MW; AA3E5A17E4904118 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 415:871-880(2002).
-!- SIMILARITY: Contains 1 RING-type zinc finger.
EMBL; AL032684; CAA21808.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       673 AA
                                                                                                                  PRINTS; PROOLOG; TYRKINASE.
ProDom; PD000001; Prot_kinase; 1.
SMART; SM00220; S.TKC; 1.
SMART; SM00219; TYRKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00069; Pkinase; 1.
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Best Local Similarity 85.،
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RESULT 36 Q9SIZ7

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Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,

A Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B.,

Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,

Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,

Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,

Boisrame A., Roszul R., Lemaire M., Lesur I., Ma L., Muller H.,

Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,

Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,

Swennene D., Tekaia F., Wesolowski-Louvel M., Westhoff E., Wirth B.,

Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,

Mincker P., Souciet J.L.;

T. "Genome evolution in yeasts.";
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
T4-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUDDITIONAL OUT STATE AND CONTROL OF SUBJECT OF SUBJECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.9%; Score 34; DB 2; Length 844;
83.3%; Pred. No. 4.3e+02;
iive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Metal-binding; Zinc; Zinc-finger.
SEQUENCE 844 AA; 95270 MW; 055B25AB3563AlCF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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FRING 2; 1.
; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TEMBLrel. 19, 01-DEC-2001 (TEMBLrel. 19, 01-DEC-2001 (TEMBLrel. 19, ORF BOC.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 83.35,
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 430:35-44(2004)
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                  NCBI_TaxID=284591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GHRPLD 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CLIB99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=80c.2;
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Q94MW0
                  NAMES OF THE PROPERTY OF THE P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.-I.,
Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
Fraser C.M., Venter J.C.,
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to sp|P31244 Saccharomyces cerevisiae DNA repair protein
RAD16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORFNames=YAL10F01232g;
Yarrowia lipolytica CL1899.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascacees; Yarrowia.
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                                                                                                                                                                                                                                                                                                                                                                                      Query Match 82.9%; Score 34; DB 2; Length 673; Best Local Similarity 71.4%; Pred. No. 3.4e+02; Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.9%; Score 34; DB 2; Length 795; 71.4%; Pred. No. 4.1e+02; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Town C.D., Kaul S.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AC007019; AAD20419.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A84608; A84608.
InterPro; IPR003877; SPRY_receptor.
Pfam; PP00622; SPRY; 1.
SWART; SW0449; SPRY; 1.
Hypothetical protein.
SEQUENCE 795 AA; 89006 MW; 07625DE69DBBFE0D CRC64;
GO; GO: 0016567; P: protein ubiquitination; IEA.
InterPro; IRR001841; Znf ring.
Pfam; PP00097; Zf-C3HC4; 1.
SMART; SM00184; RING; 1.
PROSITE; PS00518; ZF RING 1; 1.
PROSITE; PS50089; ZF RING 2; 1.
Metal-binding; Zinc; Zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Las
Hypothetical protein At2g22020.
Name-At2g22020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
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Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            || |:||
160 GHHPMDK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 GHRPLER 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GHRPLDK 7
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> Q6C3A7 Q6C3A7

CCSGBBGGGG

RESULT 37 Q6C3A7

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Paulsen I.T., James K.

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                                                            MEDLINE=21353060; PubMed=11459968; DOI=10.1073/pnas.131007398; MEDLINE=21353060; PubMed=11459968; DOI=10.1073/pnas.131007398; Mosig G., Gewin J., Luder A., Colowick N., Vo D.; Two recombination-dependent DNA replication pathways of bacteriophage T4, and their roles in mutagenesis and horizontal gene transfer."; Proc. Natl. Acad. Sci. U.S.A. 98:8306-8311(2001).
EMBL; AF374620; AAK66984.1; -.
SEQUENCE 67 AA; 8010 MW; D8C5AA794200D0A6 CRC64;
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MEDLINE=22484998; PubMed=12597275;
Raneko T., Nakamura Y., Saro S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
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MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
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DNA Res. 9:189-197(2002).
EMBL; AP005952; BAC50115.1; -.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
0RFNames=P14_0157;
Plasmodium fallciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
N.BL TAXID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bradyrhizobium japonicum.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Bradyrhizobiaceae, Bradyrhizobium.
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Pred. No. 49;
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Last annotation update)
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85.7%;
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OrderedLocusNames=blr4850;
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Best Local Similarity 85.,
6, Conservative
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Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James F. Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McRadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Fraser C.M., Barrell B., "Genome sequence of the human malaria parasite Plasmodium
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Pred. No. 1.18+02;
1; Indels
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EMBL, AE014818; AAN36769.1; -.
Hypothetical protein.
SEQUENCE 146 AA; 16861 MW; D8C846512C2379D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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6; Conservative
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